



TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-63

Query Match 90.8%; Score 506; DB 1; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60  
DB 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60  
QY 61 RFSGSGSGDTFTLTISLPEDEFAVYQCQSGSNWPHTFGGTKVEIK 107  
DB 61 RFSGSGSGDTFTLTISLPEDEFAVYQCQSGSNWPHTFGGTKVEIK 107

## RESULT 2

US-07-634-278-87  
Sequence 87, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man-Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-87

Query Match 90.8%; Score 506; DB 1; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60  
DB 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60  
QY 61 RFSGSGSGDTFTLTISLPEDEFAVYQCQSGSNWPHTFGGTKVEIK 107  
DB 61 RFSGSGSGDTFTLTISLPEDEFAVYQCQSGSNWPHTFGGTKVEIK 107

## RESULT 3

US-08-477-728-63  
Sequence 63, Application US/08477728  
Patent No. 5585089  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-728-63

Query Match 90.8%; Score 506; DB 1; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPATLSLSPGERATLSQASQSSNHLHWYQORPGQAPRLLIYRSQSSISGIPA 60



Db 1 EIVLTQSPGTLISLGERATLSRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60  
QY 61 RFGSGSGTDFLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107  
Db 61 RFGSGSGTDFLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107

RESULT 4  
US-08-477-728-87  
; Sequence 87, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-477-728-87

Query Match 90.8%; Score 506; DB 1; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSRASQISNNLHWYQKPGQAPRLLIKYRQSISGIPA 60  
Db 1 EIVLTQSPGTLISLGERATLSRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60  
QY 61 RFGSGSGTDFLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107

Db 61 RFGSGSGTDFLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107  
RESULT 5  
US-08-474-040-63  
; Sequence 63, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-474-040-63

Query Match 90.8%; Score 506; DB 1; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSRASQISNNLHWYQKPGQAPRLLIKYRQSISGIPA 60  
Db 1 EIVLTQSPGTLISLGERATLSRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60  
QY 61 RFGSGSGTDFLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107  
Db 61 RFGSGSGTDFLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107

```

; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-63

Query Match          90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. NO. 1e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY   1  EIVLTSPATLSLSPGERATLSCQASQSISNHLHWYQRPQGAPRLLLIYRSQSIGIPA 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB   1  EIVLTSPGTLSPGERATLSCRASQSISNNLHWYQQKPGQAPRLLIKAYASQSIGIPD 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY   61  RFSGSGGTDFLTITISLEPEDFAVYYCQGSWPHFTGGGTKVEIK 107
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB   61  RFSGSGGTDFLTISRLEPEDFAVYYCQGSNSWPHTFGQGTKVEIK 107
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT            8
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-87

Query Match          90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. NO. 1e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY   1  EIVLTSPATLSLSPGERATLSCQASQSISNHLHWYQRPQGAPRLLLIYRSQSIGIPA 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB   1  EIVLTSPGTLSPGERATLSCRASQSISNNLHWYQQKPGQAPRLLIKAYASQSIGIPD 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY   61  RFSGSGGTDFLTITISLEPEDFAVYYCQGSWPHFTGGGTKVEIK 107
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB   61  RFSGSGGTDFLTISRLEPEDFAVYYCQGSNSWPHTFGQGTKVEIK 107
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT            7
US-08-487-200-63
; Sequence 63, Application US/08487200

```

APPLICANT: SCHNEIDER, William P.  
 APPLICANT: LANDOLFI, Nicholas F.  
 APPLICANT: COELINGH, Kathleen L.  
 APPLICANT: SELICK, Harold E.  
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend Kourie and Crew  
 STREET: 379 Lytton Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: US  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,537  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/634,278  
 FILING DATE: 19-DEC-1990  
 APPLICATION NUMBER: US 07/590,274  
 FILING DATE: 28-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/310,252  
 FILING DATE: 13-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/290,975  
 FILING DATE: 28-DEC-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 11823-002600  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEFAX: (415) 326-2422  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-484-537-63

Query Match	90.8%	Score 506;	DB 1;	Length 107;
Best Local Similarity	90.7%	Pred. No. 1e-40;		
Matches	97;	Conservative	3;	Mismatches 7;
				Indels 0;
				Gaps 0;

61	RFSGSGSGDFLTITISLEPEFAVYVYQQSGSNPHTFGGTKEIK	107
QY		
61	RFSGSGSGDFLTITISLEPEFAVYVYQQSGSNPHTFGGTKEIK	107
DB		
1	EVVTSPTGSLSPGERATISCRASQISNNLHWYQCKPGAPRLLIYASQISGIPD	8
DB		

RESULT 10  
US-08-484-537-87

US-06-484-537-87  
; Sequence 87, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLET, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.



; FILING DATE: 27-SEPTEMBER-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6066718ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-127-721a-10

Query Match 86.2%; Score 480; DB 3; Length 127;  
Best Local Similarity 85.0%; Pred. No. 3.2e-38;  
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
  
Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRQSISGIPA 60  
Db 21 EIVLTQSPGTLSPGERATLSCRASQISGTNIHWYQKPGQAPRLLIKYASESISGIPS 80  
  
Qy 61 RFGSGSGTDTLTITISLEPEDFAVYVYQQSGSWPHTGGTKVEIK 107  
Db 81 RFGSGSGTDTLTITISLEPEDFAVYVYQQSDSWPTTFGQGTKVEIK 127

RESULT 13  
US-08-485-246A-10  
; Sequence 10, Application US/08485246A  
; Patent No. 6072035  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 6072035man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Immunoglobulin isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6072035artis Patent Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,246A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/127,721  
; FILING DATE: 27-SEPTEMBER-1993  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6072035ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-246A-10

Query Match 86.2%; Score 480; DB 3; Length 127;  
Best Local Similarity 85.0%; Pred. No. 3.2e-38;  
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
  
Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRQSISGIPA 60  
Db 21 EIVLTQSPGTLSPGERATLSCRASQISGTNIHWYQKPGQAPRLLIKYASESISGIPS 80  
  
Qy 61 RFGSGSGTDTLTITISLEPEDFAVYVYQQSGSWPHTGGTKVEIK 107  
Db 81 RFGSGSGTDTLTITISLEPEDFAVYVYQQSDSWPTTFGQGTKVEIK 127

RESULT 14  
US-08-476-176B-6  
; Sequence 6, Application US/08476176B  
; Patent No. 5958708  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 5958708man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Immunoglobulin isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5958708artis Patent Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,176B  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/127,721  
; FILING DATE: 27-SEPTEMBER-1993  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5958708ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-476-176B-6

Query Match 85.1%; Score 474; DB 2; Length 127;  
Best Local Similarity 83.2%; Pred. No. 1.2e-37;  
Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```

RESULT 15
US-08-127-721A-6
: Sequence 6, Application US/08127721A
: Patent No. 6056718
: GENERAL INFORMATION:
: APPLICANT: Hardman, No. 6056718man
: APPLICANT: Kolbinger, Frank
: APPLICANT: Saldanha, Jose
: TITLE OF INVENTION: Reshaped monoclonal antibodies against an
: TITLE OF INVENTION: immunoglobulin isotype
: NUMBER OF SEQUENCES: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6066718artis Patent and Trademark Department
:

```

US-08-127-721A-6

; Patent No. 6066718

APPLICANT: Hardman

APPLICANT: Saldanha, Jose

;; TITLE OF INVENTION: immunoglobulin isotype

CORRESPONDENCE ADDRESS: ADDRESS: NO. 606671

STREET: 39 ROUTE 10  
CITY: East Hanover

STATE: NEW JERSEY  
COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Re:

APPLICATION NUMBER: U:

; CLASSIFICATION: 424

APPLICATION NUMBER: U:

; ATTORNEY/AGENT INFORMATION  
NAME: NC 6066710-1-

; :  
REGISTRATION NUMBER:  
REFERENCE /DOCKET NUMBER:

TELEPHONE: (908) 277-

INFORMATION FOR SEO ID NO:

LENGTH: 127 amino acids

; TOPOLOGY: linear

US-08-127-721A-6

Best Local Similarity 83.1

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

[illegible]

61 PESCSCTDEFTT T T S S I F

81 RFSGSGTDETI.TISRI.F

Search\_completed: October 11,

1



220 230 240 250 260 270 280  
GACATAGTAAAGACACCTATACCTGCAAAATGAACCTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGT  
|||||  
GACATAGTAAAGACACCTATACCTGCAAAATGAACCTCTCTGAGAGCCGAGGACACAGCCGTGTATTACTGT  
220 230 240 250 260 270 280  
290 300 310 320 330 340 X  
GCAAGACATACTACGGCAGTTTCTTCTACTGGGCCAAGGACTACAGTGTACTGTTCTTAGT  
|||||  
GCAAGACATACTACGGCAGTTTCTTCTACTGGGCCAAGGACTACAGTGTACTGTTCTTAGT  
290 300 310 320 330 340 350

2. US-08-791-391A-1 (1-351)  
US-08-790-540A-3 Sequence 3, Application US/08790540A

Sequence 3, Application US/08790540A

GENERAL INFORMATION:

APPLICANT: Huse, William D.  
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/790,540A  
FILING DATE: 30-JAN-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 2405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS  
LOCATION: 1..321

Initial Score = 46 Optimized Score = 100 Significance = -0.70  
Residue Identity = 48% Matches = 125 Mismatches = 87  
Gaps = 39 Conservative Substitutions = 0

GAGATTGTGCTAACTCACTCCAGCCACCTGTCTCTCAGCCGAGGAGGCGGACTCTTTCTGCCCAG  
10 20 30 40 50 60 70

X  
CAGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGCGAGCTGGAAGG--T  
|||||  
GCCAGCCAAAGTATTAGCAACACCTACA-CTGGT---ATC-ACAAAGGCGCTGTCAAGCC-CCAAGGCTT  
80 90 X 100 110 120 130

50 60 70 80 90 100 110  
C-----CCGTG-AGACTCTCTCTGTGGAGCTGTGGATTACCTTACCTAGTATGACA-TGTCTTGGGTTTCGCC  
|||||  
CTCATCMKATATGTTCCAGTCCA-TCTCTGGGATCCCGCCAGGTTTCAGTGGCAGTGGATCAGG----GAC

140 150 160 170 180 190 200  
120 130 140 150 160 170 180  
AGGCTCCGGGC-AAGGGTCTGGAG--TGG-CTCGCAAAAGTTAGTGTGGTGGTAGCACCCTACTATTTA  
|||||  
AGATTTCACCTCACTATCTCCAGTCTGGAGCCTGAAGATTTCAGT-----CTA-----TTACTGTCAA  
210 220 230 240 250 260  
190 200 210 220 230 X 240 250  
GAGACTGTGCAG--GGCGGATTCCACATC--TCCAGAGACAAATAGTAGAACAACCCCTATACCTGCAAAATGAA  
|||||  
CAGAGTG-GCAGCTGGCC-TCACAGTTCGGAGGGGGGAGCCCAAGTGGAAATTAAG  
270 280 290 300 310 320  
260 270 280 290 300 310 320  
CTCTCTGAGAGCCGAGGACACAGCGCTGTATTACTGTGCAAGACATACTACGGCAGTTCCTTACTGCGG  
330  
CCAAGGGGACTAC



> O <  
O I O IntelliGenetics  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-08-791-391a-2.res made by jdelaval on Thu 11 Oct 101 12:13:43-PDT.

Query sequence being compared:US-08-791-391A-2 (1-117)  
Number of sequences searched: 2  
Number of scores above cutoff: 2

Results of the initial comparison of US-08-791-391A-2 (1-117) with:  
File : 08-790540.pep

100-	-----*										
N	-	-	-	-	-	-	-	-	-	-	-
U	50-	-	-	-	-	-	-	-	-	-	-
M	-	-	-	-	-	-	-	-	-	-	-
B	-	-	-	-	-	-	-	-	-	-	-
E	-	-	-	-	-	-	-	-	-	-	-
R	-	-	-	-	-	-	-	-	-	-	-
O	-	-	-	-	-	-	-	-	-	-	-
F	10-	-	-	-	-	-	-	-	-	-	-
S	-	-	-	-	-	-	-	-	-	-	-
E	5-	-	-	-	-	-	-	-	-	-	-
Q	-	-	-	-	-	-	-	-	-	-	-
U	-	-	-	-	-	-	-	-	-	-	-
E	-	-	-	-	-	-	-	-	-	-	-
N	-	-	-	-	-	-	-	-	-	-	-
C	-	-	-	-	-	-	-	-	-	-	-
E	0-	-	-	-	-	-	-	-	-	-	-
S	0	-	-	-	-	-	-	-	-	-	-
SCORE	0	13	26	39	52	65	78	91	104	117	
STDEV			0						1		

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	63	10	76.37
Times:	CPU	Total Elapsed	
	00:00:00.00	00:00:00.00	
Number of residues:		224	
Number of sequences searched:	2		
Number of scores above cutoff:	2		

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Sig. Frame
-----				

Init. Opt.

1. US-08-790-540A-2 Sequence 2, Application U 117 117 117 0.71 0
- The list of other best scores is:

Sequence Name	Description	Length	Score	Sig. Frame
-----				
2. US-08-790-540A-4 Sequence 4, Application U		107	9	30 -0.71 0

Init. Opt.

1. US-08-791-391A-2 (1-117)  
US-08-790-540A-2 Sequence 2, Application US/08790540A

Sequence 2, Application US/08790540A

GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/790.540A  
FILING DATE: 30-JAN-1997  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 2405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Initial Score = 117 Optimized Score = 117 Significance = 0.71  
Residue Identity = 100% Matches = 117 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X	10	20	30	40	50	60	70
QVQLVSGG	VQPG	GRSLR	LSCAASG	FTFSSY	DMRW	QAPG	KLEWV
QVQLVSGG	VQPG	GRSLR	LSCAASG	FTFSSY	DMRW	QAPG	KLEWV
X	10	20	30	40	50	60	70
DNSKNTLY	LQMN	SLRAED	AVYYCAR	HNYSF	AYWGQ	GTIV	TVSS
DNSKNTLY	LQMN	SLRAED	AVYYCAR	HNYSF	AYWGQ	GTIV	TVSS
X	80	90	100	110			

2. US-08-791-391A-2 (1-117)  
US-08-790-540A-4 Sequence 4, Application US/08790540A

Sequence 4, Application US/08790540A

GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human





CTCAGTATCTCCAGTCTGGAGCCTGAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAC

290 300 310 X  
ACGTTCCGAGGGGGACCAAGTGGAAATTAA  
|||||  
ACGTTCCGAGGGGGACCAAGTGGAAATTAA  
290 300 310

2. US-08-791-391A-3 (1-321)  
US-08-790-540A-1 Sequence 1, Application US/08790540A

Sequence 1, Application US/08790540A

sequence I, Application:  
GENERAL INFORMATION:

GENERAL INFORMATION: Huse, William D.

**TITLE OF INVENTION:** Anti-Alpha V Beta 3 Recombinant Human

**TITLE OF INVENTION:** Anti- $\alpha$  V  $\beta$  3 recombinant human antibodies, nucleic acids encoding same and methods of use

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

**ADDRESSEE: Campbell & Flores LLP**

**STREET:** 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

**COUNTRY:** United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

**COMPUTER:** IBM PC compatible

**OPERATING SYSTEM:** PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

**CURRENT APPLICATION DATA:**

APPLICATION NUMBER: US/08/790,540A

FILING DATE: 30-JAN-1997

**CLASSIFICATION:** 424

**ATTORNEY/AGENT INFORMATION:**

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2405

**TELECOMMUNICATION INFORMATION:**

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:

**SEQUENCE CHARACTERISTICS:**

LENGTH: 351 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

**TOPOLOGY:** linear

**FEATURE:**

NAME/KEY: CDS

LOCATION: 1..351

Initial Score	-	23	Optimized Score	-	98	Significance	-	-0.70
Residue Identity	-	50%	Matches	-	126	Mismatches	-	82
Gaps	-	40	Conservative Substitutions	-	0		-	0

GAGATTGTGCTAACTCAGTCTCCAGCCACCGTCTCTCAGCCAGGAGAAAGGGCGACTCTTTCTTGCCAG

[illegible]

140 150 160 170 180 190 200  
CTCATAGATACGTTCCCAAGTCA--TCTCTGGATCCCGCCAGGTTCACTGGCAGTGCATCAGG---GAC  
C-CCT-GGACTC--TC-CTGTGGAGCCCTCTGGATTCACCTTCAGTAGCTATGACA-TGTCTTGGGGTTCGCC

10	220	230	240	250	260	270
----	-----	-----	-----	-----	-----	-----



ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/790,540A  
 FILING DATE: 30-JAN-1997  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IX 2405  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Initial Score = 9 Optimized Score = 31 Significance = -0.70  
 Residue Identity = 30% Matches = 36 Mismatches = 69  
 Gaps = 12 Conservative Substitutions = 0

X	10	20	30	40	50	60
EIVLTQSPATLSLSPGERATLSCQAS--QSISNHLHWYQRPQGAPRLLIKYRSQISIS---- <td> </td> <td> </td> <td> </td> <td> </td> <td> </td> <td> </td>						
OVQLVESGGGVQPGPGRSLRLSCAASGFTFSYDMSWVRQAPGKGLEWVAKVSSGGGSGTYYLDTVQGRFTIS						
X	10	20	30	40	50	60
70	80	90	100			
GSQSGTDFTLTISLEPDEFAVYYC--QOQSGSWPHTFGGKVEIK						
RDNSKNTLYLQMNLSRAEDTAVYYCARHNYGS-FAYWGQGTFTVSS						
80	90	100	110			
						X

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:23:38 ; Search time 2122.65 Seconds  
(without alignments)  
2557.737 Million cell updates/sec

Title: US-08-791-391A-1  
Perfect score: 351  
Sequence: 1 CAGGTGCAGCTGGTGGAGTC.....CTACAGTGACTCTTTCTACT 351

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:.\*  
1: gb\_ba1:.\*  
2: gb\_ba2:.\*  
3: gb\_ba3:.\*  
4: gb\_in1:.\*  
5: gb\_in2:.\*  
6: gb\_in3:.\*  
7: gb\_om:.\*  
8: gb\_ov:.\*  
9: gb\_pat1:.\*  
10: gb\_pat2:.\*  
11: gb\_ph:.\*  
12: gb\_pl1:.\*  
13: gb\_pl2:.\*  
14: gb\_pl3:.\*  
15: gb\_pl4:.\*  
16: em\_ba1:.\*  
17: em\_ba2:.\*  
18: em\_fun:.\*  
19: em\_htgo\_hum:.\*  
20: em\_htgo\_inv:.\*  
21: em\_htgo\_rod:.\*  
22: em\_htg\_hum1:.\*  
23: em\_htg\_hum2:.\*  
24: em\_htg\_hum3:.\*  
25: em\_htg\_hum4:.\*  
26: em\_htg\_hum5:.\*  
27: em\_htg\_hum6:.\*  
28: em\_htg\_hum7:.\*  
29: em\_htg\_hum8:.\*  
30: em\_htg\_inv1:.\*  
31: em\_htg\_inv2:.\*  
32: em\_htg\_other:.\*  
33: em\_htg\_rod:.\*  
34: em\_hum1:.\*  
35: em\_hum2:.\*  
36: em\_hum3:.\*  
37: em\_hum4:.\*  
38: em\_hum5:.\*  
39: em\_hum6:.\*  
40: em\_hum7:.\*  
41: em\_in:.\*  
42: em\_om:.\*  
43: em\_or:.\*

44: em\_ov:.\*  
45: em\_pat:.\*  
46: em\_ph:.\*  
47: em\_pl:.\*  
48: em\_rod:.\*  
49: em\_sts:.\*  
50: em\_sy:.\*  
51: em\_un:.\*  
52: em\_vi:.\*  
53: gb\_sts1:.\*  
54: gb\_sts2:.\*  
55: gb\_sts3:.\*  
56: gb\_sy:.\*  
57: gb\_un:.\*  
58: gb\_vil:.\*  
59: gb\_vil2:.\*  
60: gb\_htg1:.\*  
61: gb\_htg2:.\*  
62: gb\_htg3:.\*  
63: gb\_htg4:.\*  
64: gb\_htg5:.\*  
65: gb\_htg6:.\*  
66: gb\_htg7:.\*  
67: gb\_htg8:.\*  
68: gb\_htg9:.\*  
69: gb\_htg10:.\*  
70: gb\_htg11:.\*  
71: gb\_htg12:.\*  
72: gb\_htg13:.\*  
73: gb\_htg14:.\*  
74: gb\_htg15:.\*  
75: gb\_htg16:.\*  
76: gb\_htg17:.\*  
77: gb\_htg18:.\*  
78: gb\_htg19:.\*  
79: gb\_htg20:.\*  
80: gb\_htg21:.\*  
81: gb\_htg22:.\*  
82: gb\_htg23:.\*  
83: gb\_htg24:.\*  
84: gb\_htg25:.\*  
85: gb\_pr1:.\*  
86: gb\_pr2:.\*  
87: gb\_pr3:.\*  
88: gb\_pr4:.\*  
89: gb\_pr5:.\*  
90: gb\_pr6:.\*  
91: gb\_pr7:.\*  
92: gb\_pr8:.\*  
93: gb\_pr9:.\*  
94: gb\_rol:.\*  
95: gb\_rol2:.\*  
96: gb\_in4:.\*  
97: gb\_pr10:.\*  
98: em\_ba3:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	351	100.0	351	9	AX060780	AX060780 Sequence
2	302.2	86.1	351	9	AX060784	AX060784 Sequence
3	268.6	76.5	482	10	I08289	I08289 Sequence 6
4	268.6	76.5	488	95	S45356	S45356 immunoglobu
5	259.6	74.0	723	10	E21535	E21535 Process for
6	259.6	74.0	761	10	E21533	E21533 Process for
7	258.8	73.7	354	94	MUSIGMUD2A	M83724 Mouse monoc
8	257.4	73.3	413	9	A38870	A38870 Sequence 24

```
9 257.4 73.3 413 9 AR013776
10 257.4 73.3 721 9 AR027762
11 257.4 73.3 721 9 AR088763
12 257.4 73.3 733 9 AR027763
13 257.4 73.3 733 9 AR088764
14 254.8 72.6 348 94 MUSIGVABB
15 254.8 72.6 351 94 MUSIGHACV
16 254.4 72.5 414 94 MMU62048
17 254 72.4 354 94 AF113106
18 254 72.4 354 94 AF113107
19 254 72.4 354 94 AF113108
20 252.4 71.9 411 10 E23343
21 252.4 71.9 411 10 E27112
22 251.8 71.7 350 94 MUSIGHNRZ
23 251.8 71.7 598 95 S55737
24 251 71.5 351 85 E09589
25 250.2 71.3 637 95 S79401
26 249.4 71.1 351 45 E09587
27 249.2 71.0 411 10 E23342
28 249.2 71.0 411 10 E27111
29 248.2 70.7 351 94 MUSIGVAAV
30 248.2 70.7 420 94 AF045519
31 248.2 70.7 420 94 AF045522
32 246.8 70.3 348 56 AF112402
33 246.6 70.3 351 94 MMU293331
34 246.6 70.3 354 94 MDIGMVE
35 246.2 70.1 351 94 MUSIGVAAU
36 246.2 70.1 480 94 MMNRK16V
37 246.2 70.1 1115 94 MMNRK16G
38 246 70.1 363 94 MDIGVAVH
39 245.8 70.0 346 94 MMU55542
40 245.4 69.9 744 56 SCO250759
41 245.2 69.9 351 94 AF098319
42 245.2 69.9 351 94 AF163750
43 245.2 69.9 384 95 U01089
44 244.8 69.7 393 94 MMU02306
45 244.8 69.7 418 9 AR022586
```

## ALIGNMENTS

```
RESULT 1
AX060780 351 bp DNA PAT 22-JAN-2001
LOCUS Sequence 1 from Patent WO0078815.
DEFINITION AX060780
ACCESSION AX060780
VERSION AX060780.1 GI:12406160
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 351)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES Location/Qualifiers
source 1..351
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>351
/codon_start=1
/transl_table=11
/protein_id="CAC24888.1"
/db_xref="GI:12406161"
/translation="OVOLVESGGGVVQPGRLSLRSCAASGTFSSYDMSWVRQAPGK
LEWAKVSSGGGVVYLDVTQGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNYG
SFAYWGQGVTVVTS"
BASE COUNT 80 a 82 c 104 g 85 t
ORIGIN
```

```
Query Match 100.0%; Score 351; DB 9; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.5e-104;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGTCCCTGAGACTC 60
DB 1 CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGTCCCTGAGACTC 60
QY 61 TCCTGTGCAGCCTCTGGATTTCACCTTCAGTACTATGACATGCTCTGGGTTGCCAGGCT 120
DB 61 TCCTGTGCAGCCTCTGGATTTCACCTTCAGTACTATGACATGCTCTGGGTTGCCAGGCT 120
QY 121 CCGGCAAGGGTCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTGTAGCAGCTACTAT 180
DB 121 CCGGCAAGGGTCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTGTAGCAGCTACTAT 180
QY 181 TTAGACACTGTGCAGGGCGGATTTCACCATCTCCAGAGACAATAGTAAGAACACCTATAC 240
DB 181 TTAGACACTGTGCAGGGCGGATTTCACCATCTCCAGAGACAATAGTAAGAACACCTATAC 240
QY 241 CTGCAAAATCAACTCTCTGAGAGCGGAGACAGACGCGTGTATTACTGTGCAAGACATAAC 300
DB 241 CTGCAAAATCAACTCTCTGAGAGCGGAGACAGACGCGTGTATTACTGTGCAAGACATAAC 300
QY 301 TACGGCAGTCTTGGCTTACTGGGCGCAAGGGACTACAGTACTGTTTCTAGT 351
DB 301 TACGGCAGTCTTGGCTTACTGGGCGCAAGGGACTACAGTACTGTTTCTAGT 351
RESULT 2
AX060784 351 bp DNA PAT 22-JAN-2001
LOCUS Sequence 5 from Patent WO0078815.
DEFINITION AX060784
ACCESSION AX060784
VERSION AX060784.1 GI:12406164
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Huse, W.D. and Wu, H.
JOURNAL Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
Patent: WO 0078815-A 5 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES Location/Qualifiers
source 1..351
/organism="Mus musculus"
/db_xref="taxon:10090"
<1..>351
/codon_start=1
/protein_id="CAC24890.1"
/db_xref="GI:12406165"
/translation="EVOLVESGGGLVQPGRLSLRSCAASGTFSSYDMSWVRQIPEKR
LEWAKVSSGGGVVYLDVTQGRFTISRDNAKNTLYLQMSLSNEDTAMYYCARHNYG
SFAYWGQGVTVVTS"
BASE COUNT 83 a 81 c 102 g 85 t
ORIGIN
```

```
Query Match 86.1%; Score 302.2; DB 9; Length 351;
Best Local Similarity 91.9%; Pred. No. 1.7e-88;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGTCCCTGAGACTCT 61
DB 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGTCCCTGAGACTCT 61
QY 62 CCTGTGCAGCCTCTGGATTTCACCTTCAGTAGTATGACATGCTCTGGGTTGCCAGGCTC 121
```



||||| 62 CCTGTGCAGCCTCTGGATTCGCTTTTCAGTAGCATGTCCTGGGTTCGCCAGATTC 121  
Db  
QY 122 CGGCAAGGCTCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181  
Db  
122 CGGAGAAGAGCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181  
QY 182 TAGACACTGTGCAGGCGCGATTCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
Db  
182 TAGACACTGTGCAGGCGCGATTCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
QY 242 TGCAATGAACCTCTGTAGAGCCGAGGACAGACCGCTGTATTACTGTGCAAGACATAACT 301  
Db  
242 TGCAATGAGCAGTCTGAACCTGTGAGGACAGACCGCATGTATTACTGTGCAAGACATAACT 301  
QY 302 ACGCAGTTTTGCTTACTGGGCGCAAGGACTACAGTCACTGTTTCT 348  
Db  
302 ACGGAGTTTTGCTTACTGGGCGCAAGGACTCTGGTCACTGTCCT 348

RESULT 3  
I08289  
LOCUS I08289 482 bp PAT 02-DEC-1994  
DEFINITION Sequence 6 from Patent EP 0380068.  
ACCESSION I08289  
VERSION I08289.1 GI:589001  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 482)  
AUTHORS Zerler,B.D.  
TITLE An expression system for production of chimeric monoclonal antibodies  
JOURNAL Patent: EP 0380068-A1 6 01-AUG-1990;  
FEATURES Location/Qualifiers  
source 1..482  
BASE COUNT 112 a 116 c 130 g 124 t  
ORIGIN

Query Match 76.5%; Score 268.6; DB 10; Length 482;  
Best Local Similarity 85.9%; Pred. No. 2e-77;  
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCGCTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61  
Db 133 AAGTGCAGCTGGTGGAGTCTGGGGAGGCGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT 192  
QY 62 CCTGTGCAGCCTCTGGATTACCTTCAGTAGCATGATGACATGCTTGGGTTCGCCAGGCTC 121  
Db 193 CCTGTGCAGCCTCTGGATTTCGCTTCAGTAGCATGATGATGCTTGGGTTCGCCAGACTC 252  
QY 122 CGGCAAGGCTCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181  
Db 253 CGGAGAAGAGCTGGAGTGGTTCGCAATATAGTAGTGGTGGTATTAACACCTACTATC 312  
QY 182 TAGACACTGTGCAGGCGCGATTCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
Db 313 CAGACACTGTGAAGGCGCGATTCACATCTCCAGAGACAATGCAAGAACACCCCTTTACC 372  
QY 242 TGCAATGAACCTCTGTAGAGCCGAGGACAGACCGCTGTATTACTGTGCAAGACATAACT 301  
Db 373 TGCAATGAGCAGTCTGAAGTCTGAGGACAGACCGCTGTATTACTGTGCAAGAGGTACG 432  
QY 302 ACGGAGTTTTGCTTACTGGGCGCAAGGACTACAGTCACTGTTTCT 348  
Db 433 GCCTCCCTTTTGTCTTACTGGGCGCAAGGACTCTGGTCACTGTCCT 479

RESULT 4  
S45356

S45356 488 bp mRNA ROD 08-MAY-1993  
LOCUS immunoglobulin heavy chain variable-anti-human IL-2R [mice, mRNA  
DEFINITION Partial, 488 nt].  
ACCESSION S45356  
VERSION S45356.1 GI:255660  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 488)  
AUTHORS Rose,B., Gillespie,A., Wunderlich,D., Kelley,K., Dzuiba,J.,  
Shedd,D., Cahill,K. and Zerler,B.  
TITLE Differential effects of a murine and chimeric mouse/human  
anti-interleukin-2 receptor antibody on human T-cell proliferation  
JOURNAL Immunology 76 (3), 452-459 (1992)  
MEDLINE 92406249  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 115041] from the original journal article.  
This sequence comes from Fig. 1b.

FEATURES  
Location/Qualifiers  
source 1..488  
/organism="Mus sp."  
/db\_xref="taxon:10095"  
gene 80..487  
/partial  
/gene="immunoglobulin heavy chain variable"  
CDS 80..487  
/partial  
/gene="immunoglobulin heavy chain variable"  
/product="immunoglobulin heavy chain variable"  
/protein\_id="AAB23305.1"  
/db\_xref="GI:255661"  
/translation="MNFGLRLFLVLTKYKCEVLVSGGLVKGPGSLKLSKAAS  
GFAFSSIDMSWVROTPEKLEWVAYISSGDNITYPTVKGRFTISRDNAKNTLYLQW  
SSLKSEDTAVYVCARRYGLPFAYVGQGLTVTSA"  
BASE COUNT 114 a 116 c 132 g 126 t  
ORIGIN

Query Match 76.5%; Score 268.6; DB 95; Length 488;  
Best Local Similarity 85.9%; Pred. No. 2e-77;  
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCGCTTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61  
Db 138 AAGTGCAGCTGGTGGAGTCTGGGGAGGCGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCT 197  
QY 62 CCTGTGCAGCCTCTGGATTACCTTCAGTAGCATGATGACATGCTTGGGTTCGCCAGGCTC 121  
Db 198 CCTGTGCAGCCTCTGGATTTCGCTTCAGTAGCATGATGATGCTTGGGTTCGCCAGACTC 257  
QY 122 CGGCAAGGCTCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181  
Db 258 CGGAGAAGAGCTGGAGTGGTTCGCAATATAGTAGTGGTGGTATTAACACCTACTATC 317  
QY 182 TAGACACTGTGCAGGCGCGATTCACATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
Db 318 CAGACACTGTGAAGGCGCGATTCACATCTCCAGAGACAATGCAAGAACACCCCTTTACC 377  
QY 242 TGCAATGAACCTCTGTAGAGCCGAGGACAGACCGCTGTATTACTGTGCAAGACATAACT 301  
Db 378 TGCAATGAGCAGTCTGAAGTCTGAGGACAGACCGCTGTATTACTGTGCAAGAGGTACG 437  
QY 302 ACGGAGTTTTGCTTACTGGGCGCAAGGACTACAGTCACTGTTTCT 348  
Db 438 GCCTCCCTTTTGTCTTACTGGGCGCAAGGACTCTGGTCACTGTCCT 484

RESULT 5  
E21535

[illegible]



Query Match 73.3%; Score 257.4; DB 9; Length 413;  
Best Local Similarity 83.9%; Pred. No. 9.6e-74;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGTGTGAGCTGTGGAGTCTGGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAGACTCT 61  
DB 64 AAGTGAAGCTGTGGAGTCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAAACTCT 123  
QY 62 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 121  
DB 124 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 183  
QY 122 CGGGCAAGGCTGTGGAGTGGGTGCGCAAGATTAGTAGTGTGTGTAGTACACTACTATT 181  
DB 184 CGGAGAAGAGCTGTGGAGTGGGTGCGCAACCATTAGTAGTGTGTAGTACACTACTATT 243  
QY 182 TAGACACTGTGAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACAACCCCTATACC 241  
DB 244 TAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACAACCCCTATACC 303  
QY 242 TGCAAATGAACCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301  
DB 304 TGCAAATGAGCACTCTGAGAGCTGTGAGGACACAGCCCTGTATTACTGTGCAAGACTACGG 363  
QY 302 ACGGCAAGTTTGTCTTACTGGGCGCAAGGACTACAGTACTGTTTCT 348  
DB 364 TAGTCCCGTTTGTCTTACTGGGCGCAAGGACTCTGGTCAACCGTCTCT 410

RESULT 10  
AR027762  
LOCUS AR027762 721 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 15 from patent US 5856456.  
ACCESSION AR027762  
VERSION AR027762.1 GI:5938582  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 721)  
AUTHORS Whitlow,M.D. and Filpula,D.R.  
TITLE Linker for linked fusion polypeptides  
JOURNAL Patent: US 5856456-A 15 05-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..721  
BASE COUNT 176 a 172 c 189 g 184 t  
ORIGIN

Query Match 73.3%; Score 257.4; DB 9; Length 721;  
Best Local Similarity 83.9%; Pred. No. 1e-73;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGTGTGAGCTGTGGAGTCTGGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAGACTCT 61  
DB 365 AAGTGAAGCTGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGCTCCCTGAAACTCT 424  
QY 62 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 121  
DB 425 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 484  
QY 122 CGGGCAAGGCTGTGGAGTGGGTGCGCAAGATTAGTAGTGTGTGTAGTACACTACTATT 181  
DB 485 CGGAGAAGAGCTGTGGAGTGGGTGCGCAACCATTAGTAGTGTGTAGTACACTACTATT 544  
QY 182 TAGACACTGTGAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACAACCCCTATACC 241  
DB 545 TAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACAACCCCTATACC 604  
QY 242 TGCAAATGAACCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301  
DB 605 TGCAAATGAGCACTCTGAGGCTGTGAGGACACAGCCCTGTATTACTGTGCAAGACTACGG 664

QY 302 ACGGCAAGTTTGTCTTACTGGGCGCAAGGACTACAGTACTGTTTCT 348  
DB 665 TAGTCCCGTTTGTCTTACTGGGCGCAAGGACTCTGGTCACTGTCTCT 711

RESULT 11  
AR088763  
LOCUS AR088763 721 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 15 from patent US 5990275.  
ACCESSION AR088763  
VERSION AR088763.1 GI:10015526  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 721)  
AUTHORS Whitlow,M.D. and Filpula,D.R.  
TITLE Linker and linked fusion polypeptides  
JOURNAL Patent: US 5990275-A 15 23-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..721  
BASE COUNT 176 a 172 c 189 g 184 t  
ORIGIN

Query Match 73.3%; Score 257.4; DB 9; Length 721;  
Best Local Similarity 83.9%; Pred. No. 1e-73; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGTGTGAGCTGTGGAGTCTGGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAGACTCT 61  
DB 365 AAGTGAAGCTGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGCTCCCTGAAACTCT 424  
QY 62 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 121  
DB 425 CTTGTGAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCTTGGTTTCGCCAGGCTC 484  
QY 122 CGGGCAAGGCTGTGGAGTGGGTGCGCAAGATTAGTAGTGTGTGTAGTACACTACTATT 181  
DB 485 CGGAGAAGAGCTGTGGAGTGGGTGCGCAACCATTAGTAGTGTGTAGTACACTACTATT 544  
QY 182 TAGACACTGTGAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACAACCCCTATACC 241  
DB 545 TAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACAACCCCTATACC 604  
QY 242 TGCAAATGAACCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301  
DB 605 TGCAAATGAGCACTCTGAGGCTGTGAGGACACAGCCCTGTATTACTGTGCAAGACTACGG 664  
QY 302 ACGGCAAGTTTGTCTTACTGGGCGCAAGGACTACAGTACTGTTTCT 348  
DB 665 TAGTCCCGTTTGTCTTACTGGGCGCAAGGACTCTGGTCACTGTCTCT 711

RESULT 12  
AR027763  
LOCUS AR027763 733 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 17 from patent US 5856456.  
ACCESSION AR027763  
VERSION AR027763.1 GI:5938583  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 733)  
AUTHORS Whitlow,M.D. and Filpula,D.R.  
TITLE Linker for linked fusion polypeptides  
JOURNAL Patent: US 5856456-A 17 05-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..733  
/organism="unknown"



LOCUS MUSIGHACV 351 bp mRNA ROD 27-APR-1993  
DEFINITION Mouse Ig H-chain mRNA VDJ-region, partial cds.  
ACCESSION M34737  
VERSION M34737.1 GI:194750  
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain; processed gene.  
SOURCE Mouse (strain BALB/c) adult spleen anti-HA hybridoma H35-D1, cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 351)  
AUTHORS Clarke, S.H., Staudt, L.M., Kavaler, J., Schwartz, D., Gerhard, W.U. and Weigert, M.G.  
TITLE V region gene usage and somatic mutation in the primary and secondary responses to influenza virus hemagglutinin  
JOURNAL J. Immunol. 144, 2795-2801 (1990)  
MEDLINE 90203619  
FEATURES  
Location/Qualifiers  
1..351  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
CDS  
<1..>351  
/note="Ig H-chain VDJ-region"  
/codon\_start=1  
/protein\_id="AAA38024.1"  
/db\_xref="GI:194751"  
/translation="EVQLVESGGGLVPGGSLKLSCAASGTFSDYMYWVROTPEKR  
LEWATISDGGSYTYPPDSVKGRFTISRDNAKNNLYLQMSLKSIEDTAMYCARYYG  
RIDYWGQGFTLVSA"  
BASE COUNT 89 a 82 c 99 g 81 t  
ORIGIN

Query Match 72.6%; Score 254.8; DB 94; Length 351;  
Best Local Similarity 83.5%; Pred. No. 6.8e-73;  
Matches 289; Conservative 0; Mismatches 57; Indels 0; Gaps 0;  
QY 2 AGGTGAGCTGTGGAGTCTGGGGAGGCGTTGTGAGCTGGAAGGTCCTGAGACTCT 61  
Db 2 AAGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCTGGAAGGTCCTGAGACTCT 61  
QY 62 CCTGTGAGCCTCTGAGTTCACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121  
Db 62 CCTGTGAGCCTCTGAGTTCACCTTCAGTAGCTATGACATGCTTGGGTCGCCAGGCTC 121  
QY 122 CGGGCAAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGTAGCAGCTACTATT 181  
Db 122 CGGAAAGAGGCTGGAGTGGGTCGCAACCATTTAGTGGTGGTGTAGCAGCTACTATC 181  
QY 182 TAGACACTGTGACAGGCGGATTCACCATCTCCAGAGACAATAGTAAGACACCCCTATACC 241  
Db 182 CAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCAAGACACCTGTACC 241  
QY 242 TGCAAATGAACTCTTGAGAGCGGAGACACAGCCCTGTATTACTGTGCAAGACATAACT 301  
Db 242 TGCAAATGAGCAGCTCTGAAGTCTGAGGACACAGCCATGATTACTGTGCAAGGTATTACT 301  
QY 302 ACGGCAGTTTGTCTTACTGGGCGCAAGGACGTACAGTACTGTTTC 347  
Db 302 ACGGTAGGATTGACTAGTGGGCGCAAGGCCACCTCTCAGGTCTC 347

Search completed: October 11, 2001, 15:09:29  
Job time: 6351 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:01:43 ; Search time 2341.88 Seconds  
(without alignments)  
1416.790 Million cell updates/sec

Title: US-08-791-391A-1

Perfect score: 351

Sequence: 1 CAGGTGCAGTGGTGGAGTC.....CTACAGTGACTGTTTCTAGT 351

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_est9.\*  
10: gb\_est10.\*  
11: gb\_est11.\*  
12: gb\_est12.\*  
13: gb\_est13.\*  
14: gb\_est14.\*  
15: gb\_est15.\*  
16: gb\_est16.\*  
17: gb\_est17.\*  
18: gb\_est18.\*  
19: gb\_est19.\*  
20: gb\_est20.\*  
21: gb\_est21.\*  
22: gb\_est22.\*  
23: gb\_est23.\*  
24: gb\_est24.\*  
25: gb\_est25.\*  
26: gb\_est26.\*  
27: gb\_est27.\*  
28: gb\_est28.\*  
29: gb\_est29.\*  
30: gb\_est30.\*  
31: gb\_est31.\*  
32: gb\_est32.\*  
33: gb\_est33.\*  
34: gb\_est34.\*  
35: gb\_est35.\*  
36: gb\_est36.\*  
37: gb\_est37.\*  
38: gb\_est38.\*  
39: gb\_est39.\*  
40: gb\_est40.\*  
41: gb\_est41.\*  
42: gb\_est42.\*  
43: gb\_est43.\*  
44: gb\_est44.\*  
45: gb\_est45.\*  
46: gb\_est46.\*  
47: gb\_est47.\*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est67:\*  
137: gb\_est68:\*  
138: gb\_est69:\*  
139: gb\_est70:\*  
140: gb\_est71:\*  
141: gb\_est72:\*  
142: gb\_est73:\*  
143: gb\_est74:\*  
144: gb\_est75:\*  
145: gb\_est76:\*  
146: gb\_est77:\*  
147: gb\_est78:\*  
148: gb\_est79:\*  
149: gb\_est80:\*  
150: gb\_est81:\*  
151: gb\_est82:\*  
152: gb\_est83:\*  
153: gb\_est84:\*  
154: gb\_est85:\*  
155: gb\_est86:\*  
156: gb\_est87:\*  
157: gb\_est88:\*  
158: gb\_est89:\*  
159: gb\_est90:\*  
160: gb\_est91:\*  
161: gb\_est92:\*  
162: gb\_est93:\*  
163: gb\_est94:\*  
164: gb\_est95:\*  
165: gb\_est96:\*  
166: gb\_est97:\*  
167: gb\_est98:\*  
168: gb\_est99:\*  
169: gb\_est100:\*  
170: gb\_est101:\*  
171: gb\_est102:\*  
172: gb\_est103:\*  
173: gb\_est104:\*  
174: gb\_est105:\*  
175: gb\_est106:\*  
176: gb\_est107:\*  
177: gb\_est108:\*  
178: gb\_est109:\*  
179: gb\_est110:\*  
180: gb\_est111:\*  
181: gb\_est112:\*  
182: gb\_est113:\*  
183: gb\_est114:\*  
184: gb\_est115:\*  
185: gb\_est116:\*  
186: gb\_est117:\*  
187: gb\_est118:\*  
188: gb\_est119:\*  
189: gb\_est120:\*

190: gb\_est121:\*  
191: gb\_est122:\*  
192: gb\_est123:\*  
193: gb\_est124:\*  
194: gb\_est125:\*  
195: gb\_est126:\*  
196: gb\_est127:\*  
197: gb\_est128:\*  
198: gb\_est129:\*  
199: gb\_est130:\*  
200: gb\_est131:\*  
201: gb\_est132:\*  
202: gb\_est133:\*  
203: gb\_est134:\*  
204: gb\_est135:\*  
205: gb\_est136:\*  
206: gb\_est137:\*  
207: gb\_est138:\*  
208: gb\_est139:\*  
209: gb\_est140:\*  
210: gb\_est141:\*  
211: gb\_est142:\*  
212: gb\_est143:\*  
213: gb\_est144:\*  
214: gb\_est145:\*  
215: gb\_est146:\*  
216: gb\_est147:\*  
217: gb\_est148:\*  
218: gb\_est149:\*  
219: gb\_est150:\*  
220: gb\_est151:\*  
221: gb\_est152:\*  
222: gb\_est153:\*  
223: gb\_est154:\*  
224: gb\_est155:\*  
225: gb\_est156:\*  
226: gb\_est157:\*  
227: gb\_est158:\*  
228: gb\_est159:\*  
229: gb\_est160:\*  
230: gb\_est161:\*  
231: gb\_est162:\*  
232: gb\_est163:\*  
233: gb\_est164:\*  
234: gb\_est165:\*  
235: gb\_est166:\*  
236: gb\_est167:\*  
237: gb\_est168:\*  
238: gb\_est169:\*  
239: gb\_est170:\*  
240: gb\_est171:\*  
241: gb\_est172:\*  
242: gb\_est173:\*  
243: gb\_est174:\*  
244: gb\_est175:\*  
245: gb\_est176:\*  
246: gb\_est177:\*  
247: gb\_est178:\*  
248: gb\_est179:\*  
249: gb\_est180:\*  
250: gb\_est181:\*  
251: gb\_est182:\*  
252: gb\_est183:\*  
253: gb\_est184:\*  
254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-re@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Prepared by: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1A9279 row: h column: 12 High quality sequence stop: 711.	
FEATURES	Location/Qualifiers 1. .1012 /organism="Mus musculus" /strain="C2ECH II" /db_xref="taxon:10090" /clone="IMAGE:4022459" /clone_lib="NCI-CGAP_Lu30" /tissue_type="tumor, metastatic to mammary" /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"	
BASE COUNT	273 a	271 c 267 g 201 t
ORIGIN		
Query Match	68.0%;	Score 238.8; DB 145; Length 1012;
Best Local Similarity	80.6%;	Pred. No. 7.5e-62;
Matches	279; Conservative	0; Mismatches 67; Indels 0; Gaps 0;
QY	2	AGGTGAGCTGTGGAGTCTGGGGAGGCGTCTGTGAGCCTGGAAGTCTCCTGAGACTCT 61
Db	102	AGGTGAGCTGTGGAGTCTGGGGAGGCGTGTAGTGAAGCTGGAGGCTCCGGAACTCT 161
QY	62	CTGTGCAGCCTCTGGATTCACCTTCAGTACGATGACATGCTCTGGTTCGCCAGGCTC 121
Db	162	CTGTGCAGCCTCTGGATTCACCTTCAGTACGATGACATGCTCTGGTTCGCCAGGCTC 221
QY	122	CGGGCAAGGCTGTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181
Db	222	CAGAAAGGGCTGTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 281
QY	182	TAGACACTGTGAGGCGGCGATTCCACCATCTCCAGAGACAATAGTAAGACACACCTATACC 241
Db	282	CAGACAGTGAAGGCGCGATTCCACCATCTCCAGAGACAATAGTAAGACACACCTATACC 341
QY	242	TGCAATGAACTCTTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGACATAACT 301
Db	342	TGCAATGAACTCTTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGACATAACT 401
QY	302	ACGGCAGTTTGTCTACTGGGCGCAAGGACATCACTGACTGTTTC 347
Db	402	ACTCCCTATGGACTACTGGGTCGAAGAACCTCAGTCCCGTCTC 447
RESULT	3	
BF452207		
LOCUS	BF452207	404 bp mRNA EST 29-DEC-2000
DEFINITION	uz85h05.y1 NCI-CGAP_Lu29 Mus musculus cDNA clone IMAGE:3675897 5' similar to SW:HV55_MOUSE P18526 IG HEAVY CHAIN V REGION 345	
PRECUSOR.	BF452207	PRECUSOR. i, mRNA sequence.
ACCESSION	BF452207	
VERSION	BF452207.1	GI:11518376
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	1 (bases 1 to 404)	
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-re@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Prepared by: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml	
FEATURES	Location/Qualifiers 1. .404 /organism="Mus musculus" /strain="C2ECH II (feral)" /db_xref="taxon:10090" /clone="IMAGE:3675897" /clone_lib="NCI-CGAP_Lu29" /tissue_type="spontaneous tumor, metastatic to mammary." Stem cell origin. /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"	
BASE COUNT	96 a	94 c 109 g 105 t
ORIGIN		
Query Match	67.5%;	Score 236.8; DB 149; Length 404;
Best Local Similarity	87.5%;	Pred. No. 2.4e-61;
Matches	259; Conservative	0; Mismatches 37; Indels 0; Gaps 0;
QY	2	AGGTGAGCTGTGGAGTCTGGGGAGGCGTGTGAGCCTGGAAGTCTCCTGAGACTCT 61
Db	107	AGGTGAGCTGTGGAGTCTGGGGAGGCGTGTAGTGAAGCTGGAGGCTCCCTGAACTCT 166
QY	62	CTGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTCTGGTTCGCCAGGCTC 121
Db	167	CTGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTCTGGTTCGCCAGGCTC 226
QY	122	CGGGCAAGGCTGTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181
Db	227	CGAAAGAGGCTGTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 286
QY	182	TAGACACTGTGAGGCGGCGATTCCACCATCTCCAGAGACAATAGTAAGACACACCTATACC 241
Db	287	TAGACAGTGTGAAGGTCGATTCCACCATCTCCAGAGACAATAGTAAGACACACCTATACC 346
QY	242	TGCAATGAACTCTTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGACAT 297
Db	347	TGCAATGAACTCTTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGACAT 402
RESULT	4	
BF45342		
LOCUS	BF45342	494 bp mRNA EST 01-FEB-2001
DEFINITION	uu72g05.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone IMAGE:3382089 5' similar to SW:HV58_MOUSE P18529 IG HEAVY CHAIN V REGION 5-76 PRECURSOR. i, mRNA sequence.	
ACCESSION	BF45342	
VERSION	BF45342.1	GI:12648749
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	1 (bases 1 to 494)	

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Other\_ESTs: uu72g05.x1  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:1087085  
Seq primer: -40RP from Gibco  
High quality sequence stop: 471.  
Location/Qualifiers  
1. .494  
/organism="Mus musculus"  
/db.xref="taxon:10090"  
/clone="IMAGE:3382089"  
/clone\_lib="Soares\_mouse\_NMGB\_bcell"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: germinal B-cell; Vector: pT7T3D-Pac  
(Pharmacia) with a modified polylinker; Site 1: Not I;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGGAGCGCCGCCGTGTTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized; constructed by Bento Soares and  
M.Fatima Bonaldo."

BASE COUNT 115 a 136 c 131 g 112 t  
ORIGIN

Query Match 67.4%; Score 236.6; DB 174; Length 494;  
Best Local Similarity 81.8%; Pred. No. 2.9e-61; Mismatches 59; Indels 5; Gaps 1;  
Matches 287; Conservative 0;  
QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 61  
DB 28 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 87  
QY 62 CCGTGCAGCCTCTGGATTCACCTTTTCAGTACCTATGATGATGCTTGGGTCGCCAGGCTC 121  
DB 88 CCGTGCAGCCTCTGGATTCACCTTTTCAGTACCTATGATGATGCTTGGGTCGCCAGGCTC 147  
QY 122 CGGCAAGGCTCTGAGTGGGTCGCAAAAGTTAGTGGTGTGCTAGCCTACTATT 181  
DB 148 CAGCAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTGGTGTGCTAGCCTACTATT 207  
QY 182 TAGACACTGTGAGGCGCGATTTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
DB 208 CAGACAGTGTGAAGGCGGATTTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATACC 267  
QY 242 TCCAAATGAACCTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACA----- 296  
DB 268 TCCAAATGACGACTCTGAAGTCTGAGGACACAGCCATGATTACTGTGCAAGCAAGGG 327  
QY 297 TAACACGCGCACTTTTGTCTTACTGGGCAAGGACTACAGTGTCTC 347  
DB 328 TACTATAGTACGACAGACTACTGGGCGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 378

RESULT 5  
BF581450 774 bp mRNA EST 12-DEC-2000  
LOCUS 602100853F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4224109 5',  
DEFINITION mRNA sequence.  
ACCESSION BF581450  
VERSION BF581450.1 GI:11655162  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 774)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9813 row: j column: 14  
High quality sequence stop: 675.  
Location/Qualifiers  
1. .774  
/organism="Mus musculus"  
/strain="FVB/N"  
/db.xref="taxon:10090"  
/clone="IMAGE:4224109"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 191 a 200 c 201 g 182 t  
ORIGIN

Query Match 66.8%; Score 234.6; DB 150; Length 774;  
Best Local Similarity 86.9%; Pred. No. 1.3e-60; Mismatches 39; Indels 0; Gaps 0;  
Matches 258; Conservative 0;  
QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 61  
DB 119 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCTCGAGACTCT 178  
QY 62 CCGTGCAGCCTCTGGATTCACCTTTTCAGTACCTATGATGATGCTTGGGTCGCCAGGCTC 121  
DB 179 CCGTGCAGCCTCTGGATTCACCTTTTCAGTACCTATGATGATGCTTGGGTCGCCAGGCTC 238  
QY 122 CGGCAAGGCTCTGAGTGGGTCGCAAAAGTTAGTGGTGTGCTAGCCTACTATT 181  
DB 239 CCGAAGAGAGGCTGGAGTGGGTCGCAAGCCATTAGTAAGGTTGGGAGCACCACCTATC 298  
QY 182 TAGACACTGTGAGGCGCGATTTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
DB 299 TAGACCTGTGAAGGCGCGATTTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATACC 358  
QY 242 TCCAAATGAACCTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATA 298  
DB 359 TCCAAATGACGACTCTGAGTCTGAGGACACAGCCCTTGTATTACTGTGCAAGACATA 415

RESULT 6  
BF582912 886 bp mRNA EST 12-DEC-2000  
LOCUS 602101361F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4224494 5',  
DEFINITION mRNA sequence.  
ACCESSION BF582912  
VERSION BF582912.1 GI:11656630  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 886)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

**COMMENT**

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9814 row: j column: 15  
High quality sequence stop: 718.

[illegible]

RESULT	7
LOCUS	AI645111
DEFINITION	Sr9g70.0.y1 Soares mouse 3NBMS Mus musculus cDNA clone IMAGE:618594 5', similar to gb:U14584 IG HEAVY CHAIN PRECURSOR V-III REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy chain v region mRNA, (MOUSE);,, mRNA sequence.
LOCUS	AI645111
DEFINITION	EST
LOCUS	469 bp
DEFINITION	mRNA
LOCUS	15-MAR-2000

ACCESSION AI645111  
 VERSION AI645111.1 GI:4723586  
 KEYWORDS EST.

**SOURCE**  
**ORGANISM**

REFERENCES

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus. 1 (bases 1 to 469)

Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone.  
This read has been verified (found to hit its original self in the  
correct orientation)

Seq primer: -40RP from Gibco.

**FEATURES**  
**SOURCE**

```

BASE COUNT
ORIGIN
1. .469
/country="Guaranteed"
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned_image="IMAGE:618594"
/clone_lib="Soares mouse 3nBMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7-3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dR) primer [5', TGTTACACTGCTGAAGTGCGGCCTGTGGTCCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7-3 vector." RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
113 a 112 c 121 g 123 t

```

```

Query Match          65.6%; Score 230.4; DB 23; Length 469;
Best Local Similarity 86.1%; Pred. No. 2.2e-59;
Matches 255: Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```

Qy	2	AGTGCAGCTGTGGAGCTCGGGGAGGCGCTTGTGCAGCCTGGAAGTCCCTCGAGACTCT	61
Db	119	ACGTGAAGCTGGTGGAGTCTGGGAGGCTGTAGTGAAGCCTGGAGGTCCTCGAAACTCT	178
Qy	62	CTGTGCAGCCTCTGGATTACACTTCAGTAGCTATGACATGTCTTGGGTTGCCAGGCTC	121
Db	179	CTGTGCAGCCTCTGGATTCACTTCAGTAGCTATGCCATGTCTTGGTTCGCCAGACTC	238
Qy	122	CGGCGAAGGCTGTGGAGTGGGTCGCAAAAGTTTAGTAGTGTGTGGTAGCACTTACTATT	181
Db	239	CAGAGAGAAGGCTGGAGTGGGTCGCATACATTAGTAGTGTGTGTATTCATCTACTATG	298
Qy	182	TAGACACTGTGCAGGCGCGATTTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC	241
Db	299	CAGACACTGTGAAGGCCGATTTCACCATCTCCAGAGACAATGCCAGGACACCCCTGTACC	358
Qy	242	TGCAAAATGAACCTCTCTGAGAGCGGAGGACACAGCCCGTGTATTACTGTGCAAGACAT	297
Db	359	TGCAAAATGACAGCTCTGAAGCTCTGAGGACACAGCCATGTATTACTGTACAAAGAT	414

## RESULTS

RESUL  
AA1702560C70/TW  
S1001

LOCUS	AA170256	823 bp	mrna	EST	16-FEB-1997
DEFINITION	ms87g10.r1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:618594				
	5' similar to gb:XI4584 IG HEAVY CHAIN PRECURSOR V-III REGION				

[illegible]



QY	122	CGGCAAGGCTCTGGAGTGGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTATT	181
Db	233	CAGAAAGGGGCTGGAGTGGGGTTGCATACATTAGTAGTGGCAGTAGTACCATCTACTATG	292
QY	182	TAGACATGTGCAGGCGCGATTCCACCATCTCCACAGACATAGTAGAACAACCCATACC	241
Db	293	CAGACACAGTGAAGGGCGGATTCCACCATCTCCAGAGACAATGCCAAGAACAACCCGTGCC	352
QY	242	TGCAAAATGAATCTCTCAGAGCGCAGGACACAGCCGTGTATTACTGTGCAAGAC---	298
Db	353	TGCAAAATGACAGTCTCAGGTCTGAGCAGACAGCGCATGTATTACTGTGCAAGCGCGGG	412
QY	299	ACTAGCGAGTTTGGCTTACTTGGGCGCAAGGACTACAGTGA	340
Db	413	GTTTCTCTGGTTTGGCTTACTTGGGCGCAAGGACTCTGGTCA	454
RESULT 13			
BF143948			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
QY			
Db			
QY			



```

Db 160 CCTGTGCAGCCTCTGGGATTCACCTTTTCAGTACTATGGAATGCATCGGTTGGTCAGGCTC 219
QY 122 CGGCAAGGGTCTGGAGTTCGCAAAAGTTAGTACTGGTGGTGGTAGCACCTACTATT 181
Db 220 CAGAGAGGGGCTGGAGTGGTTCATACATTAGTGGCAGTAGTACCATCTACTATG 279
QY 182 TAGACACTGTGCAGGGCCGAGTTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 280 CAGACACAGTGAAGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTGTCC 339
QY 242 TGCAAATGAACCTCTCTGAGAGCCGAGGACAGACAGCCGCTGTATTACTGTGCAAGACATACT 301
Db 340 TGCAAATGACCACTTAAGTCTGAGGACACAGCCGCTGTATTACTGTGCAAGGCCAGGTT 399
QY 302 ACAGCAGTCTTTGCTTACTGGGGCCAGGAGGACTACAGTGAAGTCTTTC 347
Db 400 ACTCCCTATCGGACTACTGGGGTCAAGGACCTCAGTACCCTCTC 446

RESULT 14
AW408304 440 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BK0-abj-e-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056371 5', mRNA sequence.
ACCESSION AW408304
VERSION AW408304.1 GI:6927361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 440)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
source 1..440
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3056371"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonardo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 99 a 98 c 134 g 109 t
ORIGIN

Query Match 64.6%; Score 226.8; DB 115; Length 440;
Best Local Similarity 82.1%; Pred. No. 2.7e-58;
Matches 261; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGGTGGAGTCTGGGGAGGCGTTGTGACGCTGGAAGCTCCCTGAGACTCT 61
Db 120 AGGTGACGCTGGTGGAGTCTGGGGAGGCGTTGTGACGCTGGAAGCTCCCTGAGACTCT 179

```

```

QY 62 CCTGTGCAGCCTCTGGGATTCACCTTTTCAGTACTATGATGATGTTGGTTCGCGAGGCTC 121
Db 180 CCTGTGCAGCCTCTGGGATTCACCTTTTCAGTACTATGAAATGAATGGTTCGCGAGGCTC 239
QY 122 CGGCAAGGGTCTGGAGTTCGCAAAAGTTAGTACTGGTGGTGGTAGCACCTACTATT 181
Db 240 CAGGAAAGGGGCTGGAGTGGTTCATACATTAGTACTGGTGGTAGTACCATATACG 299
QY 182 TAGACACTGTGCAGGGCCGAGTTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 300 CAGACTCTGTGAAGGGCCGAGTTCACCATCTCCAGAGACAAGCCCAAGAACTCACTGTATC 359
QY 242 TGCAAATGAACCTCTCTGAGAGCCGAGGACAGACAGCCGCTGTATTACTGTGCAAGACATACT 301
Db 360 TGCAAATGAACAGCTCAGAGCCGAGGACAGCGCTGTTTATTACTGTGCGAGAGAGGCA 419
QY 302 ACAGCAGTCTTTGCTTACT 319
Db 420 GCAGCTGGTCTTTTACT 437

RESULT 15
BF136279 718 bp mRNA EST 24-OCT-2000
LOCUS G01780988F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009197 5',
DEFINITION mRNA sequence.
ACCESSION BF136279
VERSION BF136279.1 GI:10975319
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9244 row: 0 column: 22
High quality sequence stop: 671.
FEATURES
Location/Qualifiers
source 1..718
/organism="Mus musculus"
/db_xref="CZECB II"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4009197"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 173 a 196 c 181 g 168 t
ORIGIN

Query Match 64.6%; Score 226.8; DB 145; Length 718;
Best Local Similarity 80.3%; Pred. No. 3.1e-58;
Matches 278; Conservative 0; Mismatches 67; Indels 1; Gaps 1;

QY 2 AGGTGACGCTGGTGGAGTCTGGGGAGGCGTTGTGACGCTGGAAGCTCCCTGAGACTCT 61
Db 102 AGGTGACGCTGGTGGAGTCTGGGGAGGCGTTGTGACGCTGGAAGCTCCCGAAACTCT 161

```



Search completed: October 11, 2001, 14:33:59  
Job time: 5536 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:24:48 ; Search time 177.65 Seconds  
(without alignments)  
1240.605 Million cell updates/sec

Title: US-08-791-391A-1

Perfect score: 351

Sequence: 1 CAGGTGACGTGTGGAGTC.....CTACAGTGAAGTCTTCTAGT 351

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_0601.\*  
1: /SIDS1/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDS1/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDS1/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDS1/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SIDS1/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SIDS1/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SIDS1/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SIDS1/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SIDS1/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SIDS1/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SIDS1/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SIDS1/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SIDS1/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351	100.0	351	19 AAV49820	Vitaxin antibody h
2	351	100.0	351	22 AAF28175	Vitaxin heavy chai
3	302.2	86.1	351	19 AAV49822	LM609 antibody hea
4	302.2	86.1	351	22 AAF28177	Antibody LM609 hea
5	268.6	76.5	482	11 AAQ05555	Sequence encoding
6	263.8	75.2	417	15 AAQ02804	Humanised murine K
7	263.8	75.2	417	16 AAQ07534	Humanised anti-KC-
8	259.6	74.0	582	18 AAT90020	DNA encoding heavy
9	259.6	74.0	761	20 AAX01214	Human antiFc epsil
10	259.6	74.0	770	20 AAX01216	Human antiFc epsil
11	257.4	73.3	413	15 AAQ68650	MAB A33 heavy chai

12	257.4	73.3	721	20	AAV99765	A33/212 single-cha
13	257.4	73.3	721	21	AAZ37397	Linked fusion prot
14	257.4	73.3	733	20	AAV99766	A33/218 single-cha
15	257.4	73.3	733	21	AAZ37398	Linked fusion prot
16	255	72.6	1938	19	AAV58929	A33 chimeric recep
17	252.4	71.9	411	19	AAV24243	Chimeric antibody
18	252.4	71.9	411	20	AAZ00116	Human antibody hea
19	252.4	71.9	411	21	AAZ58914	DNA seq ID No: 58
20	252.4	71.9	411	22	AAZ58914	Human antibody H c
21	252.4	71.9	411	22	AAZ58914	Human antibody H c
22	252.4	71.9	411	22	AAZ58914	Human antibody H c
23	251	71.5	351	16	AAQ96284	Human IgE receptor
24	249.4	71.1	351	16	AAQ96282	Human IgE receptor
25	249.4	71.1	351	18	AAZ90025	cDNA encoding heav
26	249.2	71.0	411	19	AAV24232	Chimeric antibody
27	249.2	71.0	411	20	AAZ00092	Mouse humanised an
28	249.2	71.0	411	21	AAZ58913	Mouse antibody H c
29	249.2	71.0	411	22	AAZ58913	Human pThrp mouse
30	249.2	71.0	411	22	AAZ58913	Human pThrp mouse
31	249.2	71.0	411	22	AAZ58913	Human pThrp mouse
32	247.4	70.5	369	19	AAV07642	anti-CD22 monoclon
33	246.8	70.3	1329	18	AAZ61281	Humanised anti-L-S
34	246.2	70.1	480	13	AAQ20070	MRK16-H chain. Ch
35	244.8	69.7	418	15	AAQ62764	Murine KC-4 immuno
36	244.8	69.7	418	15	AAQ62764	Murine KC-4 immuno
37	244.4	69.6	722	21	AAZ28996	Anti-human CTLA-4
38	244.4	69.6	729	21	AAZ28997	Anti-murine CTLA-4
39	243.6	69.4	414	21	AAZ35243	Humanised anti-ver
40	242.2	69.0	324	13	AAQ20303	B cell hybridoma l
41	241.4	68.8	357	15	AAQ66409	VH coding region o
42	240.6	68.5	360	19	AAV04636	Chimeric humanised
43	240.6	68.5	720	19	AAV04638	Chimeric humanised
44	240.2	68.4	354	18	AAZ43417	Xenograft antibody
45	240	68.4	441	18	AAZ72269	Chimeric MAB 15 PC

#### ALIGNMENTS

RESULT 1

AAV49820  
ID AAV49820 standard; DNA; 351 BP.

XX AC AAV49820;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region DNA.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;  
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;  
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
XX KW macular degeneration; osteoporosis; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers  
XX FT CDS 1..351

XX FT /\*tag= a  
XX FT /product= "vitaxin antibody heavy chain variable region"  
XX FT /note= "partial sequence, no start or stop codon given"

XX FT WO98333919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

PI	Glaser SM, Huse WD;
XX	
DR	WPI: 1998-437472/37.
DR	P-PSDB; AAW76001.
XX	
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT	Integrin - and related grafted antibodies based on murine monoclonal
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
PT	angiogenesis or restenosis
XX	
XX	Claim 3; Fig 1a; 129pp; English.
XX	
CC	This sequence encodes the vitaxin antibody variable heavy chain region.
CC	Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
CC	and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC	block integrin-mediated signal transduction. This is useful in the
CC	treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC	specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC	inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC	psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC	etc.). The antibodies contain non-murine framework regions so are
CC	suitable for use in humans. Enhanced types of LM609 have affinity more
CC	than 90 times greater than that of parent the parent antibody.
XX	
XX	Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
XX	

Query Match	100.0%;	Score 351;	DB 19;	Length 351;
Best Local Similarity	100.0%;	Pred. No. 9,9e-100;		
Matches 351;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAGGTGCAGCTGTGGAGTCTGGGGAGGCGCTGTGCAGCCTGGAAGTCCCTCAGACTC	60	
Db	1	caggTgcagctgtgTggagTctTgggggagggcgtgTgcagcctggagggccctcagactc	60	
QY	61	TCCTGTGCAGCCTCTGATTTCACCTTCAGTAGCTATGACATGCTCTGGGTTCGGCAGGCT	120	
Db	61	tccTgtcagcctctggttcaccttcagtagctatgacatgtcttgggttcgccaggt	120	
QY	121	CCGGCCAAAGGCTGTGGAGTGGGTGCCAAAAGTTAGTAGTGGTGGTGTAGCACCTACTAT	180	
Db	121	ccgggcaagggtctggagTgggtgcgaaagttagtagTggTggTgcagacctactat	180	
QY	181	TTAGACACTGTGCAGGGCCGATTCCACATCTCCAGAGACAAATAGTAAACAACCCCTATAC	240	
Db	181	ttagacaactgtgcaggggccgattccacctctccagagacaaatagtaagaaacacctatac	240	
QY	241	CTGCAATGAACCTCTCTGAGAGCCGAGGACACACCCGTGTATTACTGTGCAAGACATAAC	300	
Db	241	ctgcaaatgaactctctgagccgaggacacacggcgtgtattactgtgcgaagacataac	300	
QY	301	TACGGCAGTTTTGCTTACTGGGGCCCAAGGGACTACAGTGACTGTTTCTAGT	351	
Db	301	tacggcagttttgtcttactggggccaggagactacagtgactgtttctagt	351	

RESULT	2	
AAF28175		
ID	AAF28175	standard; DNA; 351 Bp.
XX		
XX	AAF28175;	
XX		
XX		
DT	03-APR-2001	(first entry)
XX		
XX		
DE	Vitaxin heavy chain variable region DNA.	
XX		
XX		
KW	LM609;	grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW		inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX		
XX		
OS	Unidentified.	
XX		
PN		
XX	MO200078815-Al.	
XX		

28-DEC-2000. PD  
XX XX  
23-JUN-2000; 2000WO-US17454. PF  
XX XX  
24-JUN-1999; 99US-0339922. PR  
XX XX  
(MOLE-) APPLIED MOLECULAR EVOLUTION. PA  
XX XX  
Huse WD, Wu H; PI  
XX XX  
WPI; 2001-0501110/06. DR  
XX XX  
Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis - PT  
XX XX  
Disclosure; Fig 1; 132pp; English. PS  
XX XX  
The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta\_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and osteoporosis. CC  
XX XX  
Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other; SQ

Query Match 100.0%; Score 351; DB 22; Length 351;  
Best Local Similarity 100.0%; Pred. No. 9.9e-100;  
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGTGCAGCTGTGGAGTCTGGGGAGGCGGTTGTGCAGCCTCGAAGTCCCTGAGACTC 60  
|||||  
DB 1 cagtgacgtggtgagctggtgggagggcgttgagcctggaaggtccctgagactc 60  
|||||  
QY 61 TCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATGACATGCTTGGGGTTCGCCAGGCT 120  
|||||  
DB 61 tcctgtgcagcctctggtgattcaaccttcagtagctatgacatgtctgggttgcgcaggt 120  
|||||  
QY 121 CCGGGCAAGGCTGTGGAGTGGGTGCGAAAAGTTAGTGTGCTGGTGGTAGCACCTACTAT 180  
|||||  
DB 121 ccgggcaaggctgtggagtggtggtcgaaaagttagtgggtggtgtagcacctactat 180  
|||||  
QY 181 TTAGACACTGTGCGAGGCGCCGATTCCACATCTCCAGAGACAAATAGTAAGAACACCCCTATAC 240  
|||||  
DB 181 ttgacactgtgcaggccgagattcaccatctccagagacaatagtaagaacacccctatac 240  
|||||  
QY 241 CTGCAATGAACTCTCTGCAGAGCCGAGACACACGCCGTGTATTACTGTGCAAGACATAAC 300  
|||||  
DB 241 ctgcaaatgaactctctgcagagccgagacacgcccgtgtattactgtgcaagacataac 300  
|||||  
QY 301 TACGGCAGTTTGTGCTTACTGGGGCCAAAGGGACTACAGTGACTGTGTTCTAGT 351  
|||||  
DB 301 tacggcagtttgtgcttactggggccaaagggactacagtgactgtttcttagt 351  
|||||

RESULT 3  
AAV49822  
ID ID  
AAV49822 standard; DNA; 351 BP.  
XX XX  
AAV49822; AC  
XX XX  
02-NOV-1998 (first entry) DT  
XX XX  
LM609 antibody heavy chain variable region DNA fragment. DE  
XX XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; ss.  
 XX

OS Mus sp.

XX Key Location/Qualifiers  
 XX 1. 351  
 FT CDS

FT /\*tag= a  
 FT /product= "LM609 antibody heavy chain variable region"  
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX

PS Claim 37; Fig 2a; 129pp; English.

XX This sequence encodes the LM609 antibody variable heavy chain region.  
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX

SQ Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match 86.1%; Score 302.2; DB 19; Length 351;  
 Best Local Similarity 91.9%; Pred. No. 1.5e-84;  
 Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGGGTTGTGAGCTTGGAGCTGGAAGGTCCTGAGACTCT 61

DB 2 aagtgcagctgtgagctgtgggaggttagtgagcctggaagctgagcctgagactct 61

QY 62 CCTGTGACGCTCTGAGTTCACCTTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121

DB 62 cctgtgcagcctctgagctgtgcttcagtagctatgacatgctctgggttcgccagattc 121

QY 122 CGGGCAAGGGTCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCAGCTACTATT 181

DB 122 cggagaagagctgtgagtggtgtgcgaagtagtagtggtgtgtagcactactatt 181

QY 182 TAGACACTGTGACGGCCGATTCACATCTCCAGACACAATAGTAGAAGAACCCCTATACC 241

DB 182 tagacactgtgacggccgattccacatctccagagacaatgccaaagacacccataacc 241

QY 242 TCGAATGACCTCTGTGAGACCGGAGGACACAGCCGCTGTTACTGTGCAACACATACT 301

DB 242 tgcgaatgacgctgtgagacccggagacacagccgctgttactgtgcaagacataact 301

QY 302 ACGCAGCTTTCTTACTGGGCCAGGACTACAGTGTACTGTTTCT 348  
 DB 302 acggcagctttcttactggggccaaggagactctggtcactgtctct 348

RESULT 4

AAF28177

XX AAF28177 standard; DNA; 351 BP.

AC AAF28177;

DT 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region DNA.

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX

PS Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX

SQ Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match 86.1%; Score 302.2; DB 22; Length 351;  
 Best Local Similarity 91.9%; Pred. No. 1.5e-84;  
 Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGGGTTGTGAGCTTGGAGCTGGAAGGTCCTGAGACTCT 61

DB 2 aagtgcagctgtgagctgtgggaggttagtgagcctggaagctgagcctgagactct 61

QY 62 CCTGTGACGCTCTGAGTTCACCTTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121

DB 62 cctgtgcagcctctgagctgtgcttcagtagctatgacatgctctgggttcgccagattc 121

QY 122 CGGGCAAGGGTCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGTAGCAGCTACTATT 181

DB 122 cggagaagagctgtgagtggtgtgcgaagtagtagtggtgtgtagcactactatt 181

QY 182 TAGACACTGTGCAGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
 Db 182 tagacactgtgcagggccgattccaccatctccagagacaatgccaagaacacccataacc 241  
 QY 242 TGCNAATGAACCTCTCTGAGAGCCGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301  
 Db 242 tgcaaatgagcagctggaactctgagacacagccatgtattactgtgcaagacataact 301  
 QY 302 AGGCACTTTTGTCTACTGGGCCAAGGGACTACAGTGACTGTTTCT 348  
 Db 302 acggcagcttttgtctactggggccaaggactctgtgcaactgtctct 348

RESULT 5  
 AAQ05555  
 ID AAQ05555 standard; DNA; 482 BP.  
 AC AAQ05555;  
 XX XX  
 DT 10-DEC-1990 (first entry)  
 XX XX  
 DE Sequence encoding variable region of murine AHT 54 heavy chain.  
 XX XX  
 KW Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;  
 XX XX  
 OS Mus sp.  
 XX XX  
 FH Key Location/Qualifiers  
 FT CDS 75..482  
 FT /\*tag= a  
 XX XX  
 PN EP380068-A.  
 XX XX  
 PD 01-AUG-1990.  
 XX XX  
 PF 24-JAN-1990; 90EP-0101351.  
 XX XX  
 PR 04-DEC-1989; 89US-0441702.  
 PR 24-JAN-1989; 89US-0301216.  
 XX XX  
 PA (MOLE-) MOLECULAR THERAPEU.  
 XX XX  
 PI Zerler B;  
 XX XX  
 DR WPI; 1990-232892/31.  
 DR P-PSDB; AAR06251.  
 XX XX  
 PT Expression vectors for producing chimeric monoclonal antibodies -  
 PT which express human constant region and non-human variable region  
 XX XX  
 PS Disclosure; ; p; English.  
 XX XX  
 CC MAb's comprising mouse CH and CL constant regions with human  
 CC variable regions may be used to create mouse/human hybrid MAb's,  
 CC which have a longer serum half-life. Method can be used to produce  
 CC Abs against interleukin-2 receptor and tumour necrosis factor.  
 XX XX  
 SQ Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;

Query Match 76.5%; Score 268.6; DB 11; Length 482;  
 Best Local Similarity 85.9%; Pred. NO. 4.6e-74;  
 Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2 AGGTGAGCTGTGGAGCTGTGGGAGGCGCTTGTGAGCTGGAAGGTCCCTGAGACTCT 61  
 Db 133 aagtgcagctgtgtgagctgtggggagggcttagtagcgcctggagggctccctgaaactct 192  
 QY 62 CCTGTGAGCCTCTGGATTACCTTCAGTAGCTATGACATGTCTTGGTTGCGCAGGCTC 121  
 Db 193 cctgtgcagcctctggattcgtcttcagtagcattgacatgtctgtgggttcgcagactc 252  
 QY 122 CGGCAAGGCTGTGGAGTGGGTGCGAAGCTTAGTAGTGTGTGGTAGCACCTACTATT 181

Db 253 cggagaagagcgtggagtggtcgcatcacattagtagtggtgataacacactactatc 312  
 QY 182 TAGACACTGTGCAGGCCGATTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
 Db 313 cadacactgtgaagggccgattccaccatctccagagacaatgccaagaacaccccttacc 372  
 QY 242 TGCNAATGAACCTCTCTGAGAGCCGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301  
 Db 373 tgcaaatgagcagctctgaaactctgagagacacagccgtgtattactgtgcaagaggtacg 432  
 QY 302 AGGCACTTTTGTCTACTGGGCCAAGGGACTACAGTGACTGTTTCT 348  
 Db 433 gctcccttttgtctactggggccaaggactctgtgcaactgtctct 479

RESULT 6  
 AAQ62804  
 ID AAQ62804 standard; DNA; 417 BP.  
 AC AAQ62804;  
 XX XX  
 DT 25-JAN-1995 (first entry)  
 XX XX  
 DE Humanised murine KC-4 immunoglobulin heavy chain V-region DNA.  
 XX XX  
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;  
 KW chimeric antibody; human mammary fat globule; human breast carcinoma;  
 KW murine anti-HMPG monoclonal antibody KC-4; humanised analogue; ss.  
 XX XX  
 OS Chimeric Mus musculus.  
 OS Chimeric Homo sapiens.  
 XX XX  
 FH Key Location/Qualifiers  
 FT CDS 1..416  
 FT /\*tag= a  
 FT /note= "humanised KC-4 VH chain"  
 FT mat\_peptide 58..416  
 FT /\*tag= b  
 FT /product= heavy\_chain\_V-region  
 FT /note= "humanised framework region"  
 XX XX  
 PN W09411509-A.  
 XX XX  
 PD 26-MAY-1994.  
 XX XX  
 PF 16-NOV-1993; 93WO-US11445.  
 XX XX  
 PR 16-NOV-1992; 92US-0977696.  
 PR 30-SEP-1993; 93US-0129930.  
 PR 08-OCT-1993; 93US-0134346.  
 XX XX  
 PA (CANC-) CANCER RES FUND CONTRA COSTA.  
 XX XX  
 PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;  
 XX XX  
 DR WPI; 1994-183510/22.  
 DR P-PSDB; AAR52823.  
 XX XX  
 PT New analogue peptide(s) comprising antibody variable regions -  
 PT used to develop prods. for use in the detection, diagnosis,  
 PT therapy and prevention of neoplasms  
 XX XX  
 PS Example 67; Page 91; 109pp; English.  
 XX XX  
 CC This DNA sequence encodes a humanised murine anti-human carcinoma  
 CC antibody heavy chain variable region. The humanised antibody is  
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging  
 CC of neoplastic cells. It is also of use in inhibiting the growth of  
 CC a primary or metastasised neoplasm.  
 XX XX  
 SQ Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;



PT antigenicity in humans  
 PS Disclosure; Fig 9; 26pp; Japanese.  
 XX  
 CC The present sequence, which encodes the heavy chain variable  
 CC region of the human antibody (Ab) CRA2, was used in the preparation  
 CC of a humanised or semi-chimeric monoclonal Ab (MAB), comprising  
 CC complementarity determining regions (CDR) from a murine, anti-human  
 CC high affinity immunoglobulin E (IgE) receptor, MAb. The humanised,  
 CC semi-chimeric or chimeric MAB can be used to treat or prevent  
 CC diseases, specifically allergies, associated with the receptor, and  
 CC has very low antigenicity in humans.  
 XX  
 SQ Sequence 582 BP; 133 A; 134 C; 155 G; 160 T; 0 other;

Query Match 74.0%; Score 259.6; DB 18; Length 582;  
 Best Local Similarity 84.4%; Pred. No. 3.1e-71;  
 Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGCTGGAGCTGCTGGAGCGCTGTCAGCCTGGAAGCTCCCTGAGACTCT 61  
 DB 220 aggtgcagctgctggagctgctggagcgctggtcccgccctggagactct 279  
 QY 62 CCTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121  
 DB 280 cctgtgcagctctggatctcaccttttagctatccctatccctgtctgtggctccgagctc 339  
 QY 122 CGGCGAAGGCTCTGGAGTGGTCCAAAGTTAGTAGTGGTGGTGGTACCTACTATT 181  
 DB 340 cagggaagggctggagtggtggtcccttcattagtaacgtggtgtagcacctactatc 399  
 QY 182 TAGACACTGTGCAGGCGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 241  
 DB 400 cagacactgtaaaggcgcttcacccatccagagacacgacgaactcactgtatc 459  
 QY 242 TGCAAATGAACCTCTCTGAGAGCCGAGGACAGCCGCTGTATTACTGTGCAAGACATAACT 301  
 DB 460 tgc aaatgaacagctgagagccgagacacgctgtgtattactgtcgagacataatt 519  
 QY 302 ACGCAGTTTGTCTTACTTGGGCGCAAGGACTACAGTGACTGTTC 347  
 DB 520 atggaggaatggactactg999gcaaggaccacggtcacccgtctc 565

RESULT 9  
 AAX01214  
 ID AAX01214 standard; cDNA to mRNA; 761 BP.  
 XX  
 AC AAX01214;  
 XX  
 XX 31-MAR-1999 (first entry)  
 DT  
 XX Human antiFc epsilon RI alpha chain antibody coding sequence #2.  
 DE  
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 34..753  
 FT /\*tag= a  
 FT sig\_peptide 34..90  
 FT /\*tag= b  
 FT mat\_peptide 91..750  
 FT /\*tag= c  
 XX JF11000174-A.  
 PN  
 XX 06-JAN-1999.  
 PD  
 XX  
 XX 13-JUN-1997; 97JP-0171232.  
 PF  
 XX

PR 13-JUN-1997; 97JP-0171232.  
 XX  
 PA (ASAK ) ASahi BREWERIES LTD.  
 PA (NIKK-) NIKKA WHISKEY KK.  
 PA (TORI ) TORII YAKUHIH KK.  
 PA (TSUR/) TSURA T.  
 XX  
 DR WPI; 1999-124394/11.  
 DR P-PSDB; AAW73874.  
 XX  
 PT Preparing an antibody Fab fragment using yeast - in high yield  
 XX  
 PS Claim 6; Page 7; 13pp; Japanese.  
 XX  
 CC This sequence encodes a human antiFc epsilon RI alpha chain antibody,  
 CC produced using the method of the invention. The method is for preparing  
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host  
 CC cell. The method can prepare an antibody Fab fragment cost efficiently  
 CC and in high yield.  
 XX  
 SQ Sequence 761 BP; 166 A; 228 C; 206 G; 161 T; 0 other;

Query Match 74.0%; Score 259.6; DB 20; Length 761;  
 Best Local Similarity 84.4%; Pred. No. 3.4e-71;  
 Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGCTGGAGCTGCTGGAGCGCTGTCAGCCTGGAAGCTCCCTGAGACTCT 61  
 DB 92 aggtgcagctgctggagctgctggagcgctggtcccgccctggagactct 151  
 QY 62 CCTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121  
 DB 152 cctgtgcagctctggatctcaccttttagctatccctatccctgtctgtggctccgagctc 211  
 QY 122 CGGCGAAGGCTCTGGAGTGGTCCAAAGTTAGTAGTGGTGGTGGTACCTACTATT 181  
 DB 212 cagggaagggctggagtggtggtcccttcattagtaacgtggtgtagcacctactatc 271  
 QY 182 TAGACACTGTGCAGGCGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 241  
 DB 272 cagacactgtaaaggcgcttcacccatccagagacacgacgaactcactgtatc 331  
 QY 242 TGCAAATGAACCTCTCTGAGAGCCGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301  
 DB 332 tgc aaatgaacagctgagagccgagacacgctgtgtattactgtcgagacataatt 391  
 QY 302 ACGCAGTTTGTCTTACTTGGGCGCAAGGACTACAGTGACTGTTC 347  
 DB 392 atggaggaatggactactg999gcaaggaccacggtcacccgtctc 437

RESULT 10  
 AAX01216  
 ID AAX01216 standard; cDNA to mRNA; 770 BP.  
 XX  
 AC AAX01216;  
 XX  
 XX 31-MAR-1999 (first entry)  
 DT  
 XX Human antiFc epsilon RI alpha chain antibody coding sequence #4.  
 DE  
 XX AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 34..762  
 FT /\*tag= a  
 FT sig\_peptide 34..99  
 FT /\*tag= b  
 FT mat\_peptide 100..759  
 FT /\*tag= c  
 FT



XX JPI1000174-A.  
 XX 06-JAN-1999.  
 XX 13-JUN-1997; 97JP-0171232.  
 XX 13-JUN-1997; 97JP-0171232.  
 XX (ASAK ) ASAHI BREWERIES LTD.  
 XX (NIKK-) NIKKA WHISKEY KK.  
 XX (TORI ) TORII YAKUHHN KK.  
 XX (TSUR/) TSURA T.  
 XX WPI; 1999-124394/11.  
 XX P-PSDB; AAW73876.  
 XX  
 XX Preparing an antibody Fab fragment using yeast - in high yield  
 XX  
 XX Claim 6; Page 9-10; 13pp; Japanese.  
 XX  
 XX This sequence encodes a human antiFc epsilon RI alpha chain antibody,  
 CC produced using the method of the invention. The method is for preparing  
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host  
 CC cell. The method can prepare an antibody Fab fragment cost efficiently  
 CC and in high yield.  
 XX  
 XX Sequence 770 BP; 172 A; 223 C; 205 G; 170 T; 0 other;  
 SQ  
 Query Match 74.0%; Score 259.6; DB 20; Length 770;  
 Best Local Similarity 84.4%; Pred. No. 3.4e-71;  
 Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
 QY 2 AGGTCACCTGGTGGAGCTGCGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTCT 61  
 Db 101 aggtgcagctggtgagctggtgagctggtgagctggtgagctggtgagctggtgagct 160  
 QY 62 CTGTGACGCTCTGAGTTCACCTTCAGTATGATGATGATGATGATGATGATGATGATGAT 121  
 Db 161 cctgtgcagctctggtgagctggtgagctggtgagctggtgagctggtgagctggtgagct 220  
 QY 122 CGGCAAGGCTGTGAGTGGGTGCGAAAGTTAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 181  
 Db 221 cagggaaggctggtgagctggtgagctggtgagctggtgagctggtgagctggtgagct 280  
 QY 182 TAGACACTGTGAGGCGGATTCACCTCTCCAGAGACAATAGTAAAGAACCCCTATACC 241  
 Db 281 cagacactgtaaggccgagctgagctgagctgagctgagctgagctgagctgagctgagct 340  
 QY 242 TGCAATGAACCTCTGTGAGCGGAGGACACAGCGGTGTATGATGATGATGATGATGATGAT 301  
 Db 341 tgcataatgaacactctgtgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 400  
 QY 302 ACGGCGAGTTTGTCTTACGTGGGCGGAGGAGTACAGTGTGAGTGTGAGTGTGAGTGT 347  
 Db 401 atggagggaatgactgactgactgactgactgactgactgactgactgactgactgactgact 446  
 RESULT 11  
 ID AAQ68650  
 XX AAQ68650 standard; DNA; 413 BP.  
 XX  
 AC AAQ68650;  
 XX  
 XX 13-FEB-1995 (first entry)  
 DE  
 DE MAB A33 heavy chain coding sequence.  
 KW Polymerase chain reaction; primer; amplify; PCR; variable region; light;  
 KW heavy; chains; VH; humanised; antibody; vectors; expression; human;  
 KW secretion; A33; Fab; (gamma/delta/cys); pcg16; ompa signal; C-kappa;  
 KW pskomp; pmrr055; CH1 domains; hinge; deltaCys; pmrr022; pro109;

antigen; diagnosis; treatment; colorectal cancer; metastases; ss.  
 Chimeric - Mus musculus.  
 Chimeric - Homo sapiens.  
 Key Location/Qualifiers  
 primer\_bind 1..32 /\*tag= a  
 CDS 6..413 /\*tag= b  
 sig\_peptide 6..62 /\*tag= c  
 mat\_peptide 63..413 /\*tag= d  
 primer\_bind 396..413 /\*tag= e  
 W09413805-A.  
 23-JUN-1994.  
 10-DEC-1993; 93WO-GB02529.  
 10-DEC-1992; 92GB-0025853.  
 22-JUL-1993; 93GB-0015249.  
 (CLLT ) CELLTech LTD.  
 Adair JR, King DJ, Owens RJ;  
 WPI; 1994-217881/26.  
 P-PSDB; AAR56962.  
 Humanised antibodies raised against A33 antigen - are used for  
 diagnosis or treatment of colorectal tumours and metastases  
 Example 1; Fig 3(ii); 90pp; English.  
 The sequences given in AAQ68649-50 encode the light and heavy chain  
 variable regions (VH and VL) of the humanised anti-A33 antibody of  
 the invention. These fragments were produced by PCR using the primer  
 sequences given in AAQ68624-48. The amplified fragments were used in  
 the construction of vectors for the expression and secretion of the  
 chimeric humanised A33. The amplified products were cleaved with BstBI  
 and SphI for the light chain and HindIII and ApaI for the heavy chain.  
 These fragments were cloned into the human kappa light chain acceptor  
 vector, pmrr15.1, and the human heavy chain, IgG1, acceptor vector,  
 pmrr011 respectively, to give chimeric expression vector pro108 for the  
 light chain and pro107 for the heavy chain. Proteins which bind the A33  
 antigen can be used in the diagnosis or treatment of colorectal cancers  
 and metastases.  
 Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;  
 Query Match 73.3%; Score 257.4; DB 15; Length 413;  
 Best Local Similarity 83.9%; Pred. No. 1.3e-70;  
 Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
 QY 2 AGGTCACGCTGTGAGTGTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTCT 61  
 Db 64 aagtgaagctggtgagctggtgagctggtgagctggtgagctggtgagctggtgagct 123  
 QY 62 CCGTGTGACGCTCTGAGTTCACCTTCAGTATGATGATGATGATGATGATGATGATGAT 121  
 Db 124 cctgtgcagctctggtgagctggtgagctggtgagctggtgagctggtgagctggtgagc 183  
 QY 122 CGGCAAGGCTGTGAGTGGGTGCGAAAGTTAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 181  
 Db 184 cggagaagagctggtgagctggtgagctggtgagctggtgagctggtgagctggtgagc 243  
 QY 182 TAGACACTGTGAGGCGGAGTTCACCTCTCCAGAGACAATAGTAAAGAACCCCTATACC 241  
 Db 182 TAGACACTGTGAGGCGGAGTTCACCTCTCCAGAGACAATAGTAAAGAACCCCTATACC 241

Db	244	tagacagtgtaaggccgattcaccatctccagagacagtgccaggaacacacctatacc	303
Qy	242	TGCAAAATGAACACTCTCTGAGAGCCGAGGACACACGCCGTGTATTACTGTGCAAGACATAACT	301
Db	304	tgcnaaatgagcagtcgtgaggtctgaggacaacgccttgtattactgtcacgcgaactacgg	363
Qy	302	ACGGCAGTTTTTGTCTACTGGGGCCAAGGACTACAGTGACTGTTTCT	348
Db	364	tagtcccgtttgtactggcgcaaggactctgtgccccgtctct	410
 RESULT 12 AAV99765 ID AAV99765 standard; DNA; 721 BP. XX AC AAV99765; DT DT (first entry) XX DE 23-MAR-1999 XX DE A33/212 single-chain Fv coding sequence.			
KW	Linker;	fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;	
KW	multichain protein;	immunoglobulin; single chain antibody Fv; cancer;	
KW	aggregation; ds.		
XX	Synthetic.		
OS	Key	Location/Qualifiers	
FX	CDS	1..711	
FT		/*tag= a	
FT		/product= "A33/212 scFv"	
FT		/note= "the start codon is not indicated"	
FT	misc_feature	1..321	
FT		/*tag= b	
FT		/note= "sequence coding for A33 VL region"	
FT	misc_feature	322..363	
FT		/*tag= c	
FT		/note= "sequence coding for peptide linker 212"	
FT	misc_feature	364..708	
FT		/*tag= d	
FT		/note= "sequence coding for A33 Vh region"	
XX	US5856456-A.		
PX	05-JAN-1999.		
XX	07-APR-1994;	94US-0224591.	
PR	07-APR-1994;	94US-0224591.	
PR	20-NOV-1992;	92US-0980529.	
PR	15-JAN-1993;	93US-0002845.	
XX	{ENZO-} ENZON INC.		
XX	Filpula DR,	Whitlow MD;	
PI	WPI;	1999-105193/09.	
DR	p-PSDB;	AAW95440.	
XX	DNA encoding fusion polypeptide including protease resistant linker		
PT	- for making single-chain Fv antibody fragments, e.g for diagnosis		
PT	and treatment of cancer		
XX	Disclosure; Fig 12; 39pp; English.		
XX	The invention is directed to a novel peptide linker useful for connect-		
CC	ing polypeptide constituents into a novel linked fusion polypeptide. The		
CC	peptide linker includes at least one XP motif (where X is a charged		
CC	amino acid) and includes any of these sequences (GSTSGGPGSGSGEGSTKG		
CC	GTSGLXPSGSGSTKG; or GSTSGKSEKKG) to inhibit its proteolysis by		
CC	subtilisin or trypsin. DNA molecules encoding fusion polypeptides		
CC	'containing two polypeptides, derived from the same multichain protein		
CC	'the immunoglobulin (Ig) superfamily and a peptide linker as above, are		

PS Example; Fig 12; 42pp; English.

XX This sequence encodes a linked fusion protein containing the

CC amino acid linker of the invention. The linkers are used for connecting

CC constituent polypeptides to form novel linked fusion polypeptides.

CC Polypeptides derived from any protein can be connected, in particular

CC multichain protein or protein complexes e.g. enzymes, members of the

CC immunoglobulin superfamily, hormones, DNA-binding proteins. The linker

CC provides fusion proteins which have greater stability and are less

CC susceptible to aggregation.

XX Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;

SQ

Query Match 73.3%; Score 257.4; DB 21; Length 721;

Best Local Similarity 83.9%; Pred. NO. 1.6e-70;

Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGGTGGAGTCTGGGGAGCGGTGTGTCAGCCTGGAGGTCCTGAGACTCT 61

DB 365 aagtgagctgtgagctgtgggagccttagtgaaagcctggaggtccctgaaactct 424

QY 62 CCTGTGACGCTCTGACCTTCACCTTCAGTAGTATGACATGCTTTGGTTCGCCAGGCTC 121

DB 425 cctgtgcagccttgagctgttccttcagtaacctatgacatgtcttgggtccagactc 484

QY 122 CGGCAAGGCTCGAGTGGCTGCAAGAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGT 181

DB 485 cggagagagcctggagcgggttcgcaaccattagtagtgggtgggtgggtgggtgggt 544

QY 182 TAGACACTGTGACGGCGGATTCACATCTCCAGACACAATAGTAAAGACACCTATACC 241

DB 545 tagacagtgaagggcagctaccattccagagacagtgccaggaacacctatacc 604

QY 242 TCCAAATGAATCTCTGAGACCGGAGGACAGCGGTGTATTTACTGTGCAAGACATACT 301

DB 605 tgcgaatgagcagctgagctgagctgagggacagcggctgtattactgtgcacgactcgg 664

QY 302 ACGGCGAGTTTGTCTTACTGGGCGCAAGGACTACAGTCACTGTTTCT 348

DB 665 tagtcccgcttgctacttggggccaaaggagcctggtcactgtctct 711

RESULT 14

ID AAV9766 standard; DNA; 733 BP.

AC AAV9766;

XX

DT 23-MAR-1999 (first entry)

XX

DE A33/218 single-chain Fv coding sequence.

XX

KW Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;

KW multichain protein; immunoglobulin; single chain antibody Fv; cancer;

KW aggregation; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 1..711

FT /tag= a

FT /product= "A33/218 scFv"

FT /note= "the start codon is not indicated"

FT misc\_feature 1..321

FT /tag= b

FT /note= "sequence coding for A33 V1 region"

FT misc\_feature 322..375

FT /tag= c

FT /note= "sequence coding for peptide linker 218"

FT misc\_feature 376..708

FT /tag= d

FT /note= "sequence coding for A33 Vh region"

XX US5856456-A.

PN 05-JAN-1999.

PD

XX 07-APR-1994; 94US-0224591.

PF

XX 07-APR-1994; 94US-0224591.

PR 20-NOV-1992; 92US-0980529.

PR 15-JAN-1993; 93US-0002845.

XX

PA (ENZO-) ENZON INC.

XX

PI Filpula DR, Whitlow MD;

XX

DR WPI; 1999-105193/09.

DR P-PSDB; AAW95441.

XX

PT DNA encoding fusion polypeptide including protease resistant linker

PT - for making single-chain Fv antibody fragments, e.g for diagnosis

PT and treatment of cancer

PS Disclosure; Fig 13; 39pp; English.

XX

CC The invention is directed to a novel peptide linker useful for connecting

CC polypeptide constituents into a novel linked fusion polypeptide. The

CC peptide linker includes at least one XP motif (where X is a charged

CC amino acid) and includes any of these sequences (GSTSGXPGSGSGSGTKG;

CC GSTSGXPGSGSGTKG; or GSTSGKSGKG) to inhibit its proteolysis by

CC subtilisin or trypsin. DNA molecules encoding fusion polypeptides

CC containing two polypeptides, derived from the same multichain protein of

CC the immunoglobulin (Ig) superfamily and a peptide linker as above, are

CC particularly used to prepare single chain antibody Fv fragments (scFv),

CC polypeptide containing the specified linkers is proteolytically stable

CC aggregation, while residue X improves solubility. The present sequence

CC represents the nucleotide sequence of a A33/218 scFv fragment.

XX

SQ Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 73.3%; Score 257.4; DB 20; Length 733;

Best Local Similarity 83.9%; Pred. NO. 1.6e-70;

Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGGTGGAGTCTGGGGAGCGGTGTGTCAGCCTGGAGGTCCTGAGACTCT 61

DB 377 aagtgagcctgtgagctgtgggagccttagtgaaagcctggaggtccctgaaactc 436

QY 62 CCTGTGACGCTCTGACCTTCACCTTCAGTAGTATGACATGCTTTGGTTCGCCAGGCTC 121

DB 437 cctgtgcagcctcttgattcgtttcagtaacctagacatgcttgggttcgccagactc 496

QY 122 CGGCAAGGCTGTGAGTGGGTGCGAAAGTTAGTAGTGGTGGTGGTGGTGGTGGTGGT 181

DB 497 cggagagagcctgagctgggtgcgaaccttagtagtgggtgggttagtacactactatt 556

QY 182 TAGACACTGTGACGGCGGATTCACCATCTCCAGACACAATAGTAGAACACACCTATACC 241

DB 557 tagacagtgtgaagggcggattccacctctccagagcagtgccagggaacacctatacc 616

QY 242 TCCAAATGAATCTCTGAGACCGGAGGACACAGCGGTGTATTTACTGTGCAAGACATACT 301

DB 617 tgcgaatgagcagctgagctgagggacagcggcctgtattactgtgcacgactcgg 676

QY 302 ACGGCGAGTTTGTCTTACTGGGCGCAAGGACTACAGTCACTGTTTCT 348

DB 677 tagtcccgcttgctacttggggccaaaggagcctcgtgctcactgtctct 723

RESULT 15

AAZ37398

Db 677 tagtcccgtttgccttactggggccaaagggaactctgtgtaactgtctct 723

Search completed: October 11, 2001, 15:12:35  
Job time: 6467 sec

ID AAZ37398 standard; DNA; 733 BP.  
XX AAZ37398;  
XX  
XX  
DT 08-FEB-2000 (first entry)  
XX  
XX Linked fusion protein A33/218 sfv coding sequence.  
DE  
XX  
KW Fusion protein; linker; linked fusion polypeptide; multichain protein;  
KW protein complex; antibody; ss.  
XX  
XX Synthetic.  
XX  
XX US5990275-A.  
XX  
XX 23-NOV-1999.  
XX  
XX 10-SEP-1997; 97US-0926789.  
XX  
XX 07-APR-1994; 94US-0224591.  
XX  
XX 20-NOV-1992; 92US-0980529.  
XX  
XX 15-JAN-1993; 93US-0002845.  
XX  
XX (ENZO-) ENZON INC.  
XX  
XX Filpula DR, Whitlow MD;  
XX  
XX WPI; 2000-022812/02.  
XX  
XX P-PSDB; AAY54837.  
XX  
XX Peptide linkers, linked fusion polypeptides containing the linkers and  
XX their preparation -  
XX  
XX Example; Fig 13; 42pp; English.  
XX  
XX This sequence encodes a linked fusion protein containing the  
XX amino acid linker of the invention. The linkers are used for connecting  
XX constituent polypeptides to form novel linked fusion polypeptides.  
XX Polypeptides derived from any protein can be connected, in particular  
XX multichain protein or protein complexes e.g. enzymes, members of the  
XX immunoglobulin superfamily, hormones, DNA-binding proteins. The linker  
XX provides fusion proteins which have greater stability and are less  
XX susceptible to aggregation.  
XX  
XX Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 73.3%; Score 257.4; DB 21; Length 733;  
Best Local Similarity 83.9%; Pred. No. 1.6e-70;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTGCAGCCTGGAAGTCCCTGAGACTCT 61  
Db 377 aagtgaagcttggagtgctgggggagcttagtgagcctgagggtccctgaaactct 436  
QY 62 CCTGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121  
Db 437 cctgtgcagcctctggagtcgcttcagctacatgacatgctctgtggttcgcagactc 496  
QY 122 CGGGCAAGGCTCGGAGTGGTGCAGAAAGTTAGTAGTGGTGTAGCACCTACTATT 181  
Db 497 cggagaagaggctcggagtggtgcgaaccattagtagtggtggttagtaccactactatt 556  
QY 182 TAGACACTGTGACGGCCGATTACCATCTCCAGAGACAATAGTAAGAACCCCTATACC 241  
Db 557 tagacagtgtgaaggccgattccaccatctccagagacagtgcaggaacacccatacc 616  
QY 242 TGCAAATGACTCTCTGAGAGCCGAGGACACAGCCGCTGTATTACTGTGCAAGACATACT 301  
Db 617 tgcgaatgacagctgtgaggtctgagacacgacgacctgtattactgtgcaccgactacg 676  
QY 302 ACGGCAGTTTGTCTTACTGTTGGGCAAGGACTACAGTGACTGTCTTCT 348



THIS PAGE BLANK (USPTO)

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 13:50:53 ; Search time 87.94 Seconds  
(without alignments)  
755.608 Million cell updates/sec

Title: US-08-791-391a-1

Perfect score: 351

Sequence: 1 CAGGTGACGTGCTGGAGTC.....CTACAGTGACTGTTTCTAGT 351

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_NA.\*
- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
  - 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
  - 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
  - 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
  - 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
  - 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.4	73.3	413	1	US-08-253-877C-56
2	257.4	73.3	413	2	US-08-432-164A-56
3	257.4	73.3	721	2	US-08-224-591-15
4	257.4	73.3	721	2	US-08-926-789-15
5	257.4	73.3	733	2	US-08-224-591-17
6	257.4	73.3	733	2	US-08-926-789-17
7	246.8	70.3	405	4	US-08-579-378A-19
8	246.8	70.3	1329	5	PCT-US96-13152-3
9	244.8	69.7	418	1	US-07-977-696C-27
10	244.8	69.7	418	1	US-08-129-930B-27
11	240.6	68.5	360	2	US-08-672-176A-5
12	240.6	68.5	720	2	US-08-672-176A-5
13	239.8	68.3	357	1	US-08-475-000-15
14	239.8	68.3	357	2	US-08-483-199-15
15	239.8	68.3	357	2	US-08-484-508-15
16	238.2	67.9	445	1	US-08-053-171-10
17	238.2	67.9	491	1	US-08-053-171-6
18	237.2	67.6	717	2	US-08-553-497A-17
19	236.6	67.4	717	2	US-07-956-399-3
20	235.6	67.1	357	1	US-08-331-398A-21
21	235.6	67.1	357	1	US-08-207-996-26
22	235.6	67.1	357	2	US-08-760-840A-26
23	235.6	67.1	357	2	US-08-760-840A-27
24	235.6	67.1	357	2	US-08-331-397B-21
25	235.6	67.1	357	2	US-08-759-804A-21
26	235.6	67.1	357	3	US-09-266-119-26
c 27	235.6	67.1	357	3	US-09-266-119-27

28	235.6	67.1	375	1	US-08-331-398A-59	Sequence 59, Appl
29	235.6	67.1	375	2	US-08-331-397B-59	Sequence 59, Appl
30	235.6	67.1	375	2	US-08-759-804A-58	Sequence 58, Appl
31	235.6	67.1	738	1	US-08-331-398A-31	Sequence 31, Appl
32	235.6	67.1	738	2	US-08-331-397B-31	Sequence 31, Appl
33	235.6	67.1	738	2	US-08-759-804A-31	Sequence 31, Appl
34	235.4	67.1	923	5	PCT-US94-07659-1	Sequence 1, Appl
35	235	67.0	354	4	US-08-487-761-14	Sequence 14, Appl
36	234.8	66.9	417	1	US-08-398-613A-21	Sequence 21, Appl
37	234.8	66.9	417	1	US-08-398-612A-21	Sequence 21, Appl
38	234.8	66.9	417	1	US-08-398-611A-21	Sequence 21, Appl
39	234.8	66.9	417	1	US-08-396-851A-21	Sequence 21, Appl
40	234.8	66.9	417	2	US-08-491-334A-21	Sequence 21, Appl
41	234.8	66.9	417	3	US-09-027-449-18	Sequence 18, Appl
42	234.8	66.9	417	3	US-08-804-444A-18	Sequence 18, Appl
43	234.8	66.9	417	3	US-09-026-985-18	Sequence 18, Appl
44	234.8	66.9	756	1	US-08-398-613A-29	Sequence 29, Appl
45	234.8	66.9	756	1	US-08-398-612A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-253-877C-56  
; Sequence 56, Application US/08253877C  
; Patent No. 5773001  
; GENERAL INFORMATION:  
; APPLICANT: Hamann, Philip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,877C  
; FILING DATE: 03-JUN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 32,368  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3246  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 413 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 6..413  
US-08-253-877C-56

Query Match 73.3%; Score 257.4; DB 1; Length 413;  
Best Local Similarity 83.9%; Pred. No. 3.7e-77;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
QY 2 AGGTGAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAGACTCT 61  
DB 64 AAGTGAAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAAACTCT 123  
QY 62 CCGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121  
DB 124 CCGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 183  
QY 122 CGGGCAAGGCTCTGGAGTGGTGGCGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181  
DB 184 CGGAGAAGGCTGGAGTGGTGGCGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 243  
QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACAATAGTAGAAGACACCCCTATAC 241  
DB 244 TAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACAGTCCAGGAACACCCCTATAC 303  
QY 242 TGCAGTGAAGTCTCTGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301  
DB 304 TGCAGTGAAGTCTCTGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363  
QY 302 ACGGAGTGTGCTTACTGGGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348  
DB 364 TAGTCCCGTTGCTTACTGGGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410

RESULT 2  
US-08-452-164A-56  
; Sequence 56, Application US/08452164A  
; Patent No. 5877296  
; GENERAL INFORMATION:  
; APPLICANT: Hamann, Philip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Home Products Corporation  
; STREET: One Campus Drive  
; CITY: Parsippany  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/452,164A  
; FILING DATE: 26-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 32,368-04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-683-2158  
; TELEFAX: 201-683-4117  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 413 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 6..413  
; US-08-452-164A-56  
Query Match 73.3%; Score 257.4; DB 2; Length 413;  
Best Local Similarity 83.9%; Pred. No. 3.7e-77;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
QY 2 AGGTGAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAGACTCT 61  
DB 64 AAGTGAAGCTGGTGGAGTCTGGGGAGGCGTTGTGAGCCTGGAAGTCCCTGAAACTCT 123  
QY 62 CCGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121  
DB 124 CCGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 183  
QY 122 CGGGCAAGGCTCTGGAGTGGTGGCGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181  
DB 184 CGGAGAAGGCTGGAGTGGTGGCGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 243  
QY 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACAATAGTAGAAGACACCCCTATAC 241  
DB 244 TAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACAGTCCAGGAACACCCCTATAC 303  
QY 242 TGCAGTGAAGTCTCTGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301  
DB 304 TGCAGTGAAGTCTCTGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363  
QY 302 ACGGAGTGTGCTTACTGGGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348  
DB 364 TAGTCCCGTTGCTTACTGGGGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410

RESULT 3  
US-08-224-591-15  
; Sequence 15, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,591  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600



```
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
US-08-224-591-15

Query Match          73.3%; Score 257.4; DB 2; Length 721;
Best Local Similarity 83.9%; Pred. No. 4.8e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY  2 AGGTGCAGCTGGTGGAGTCTGGGGGAGCGGTGTGCAGCCTGGAAGGTCCCTGAGACTCT 61
Db  365 AAGTGAAGCTTGTGGAGTCTGGGGGAGCGGTGTGCAGCCTGGAAGGTCCCTGAAACTCT 424

QY  62 CCTGTGAGCTCTGGAGTCTGGAGTCTGCAAAAGTGTAGTGTGGTGGTAGCACCCTACTATT 181
Db  425 CCTGTGAGCTCTGGAGTCTGGAGTCTGCAAAAGTGTAGTGTGGTGGTAGCACCCTACTATT 544

QY  122 CGGCAAGAGCTCTGGAGTCTGGAGTCTGCAAAAGTGTAGTGTGGTGGTAGCACCCTACTATT 181
Db  485 CGGCAAGAGCTCTGGAGTCTGGAGTCTGCAAAAGTGTAGTGTGGTGGTAGCACCCTACTATT 544

QY  182 TAGACACTGTGCAGGCGCGGATTCACCATCTCCAGAGACAATAGTAGTGTGGTGGTAGCACCCTACTATT 181
Db  545 TAGACACTGTGCAGGCGCGGATTCACCATCTCCAGAGACAATAGTAGTGTGGTGGTAGCACCCTACTATT 544

QY  242 TGCAAATGAAGTCTCTGAGAGCCGAGGACAGCCGCTGTATTACTGTGCAAGACATAACT 301
Db  605 TGCAAATGAGCAGTCTGAGGTCTGAGGACAGCGGCTGTATTACTGTGCAAGACATAACT 301

QY  302 ACGCAGTTTTCCTTACTTGGGGCCCAAGGACTACAGTCACTGCTTCT 348
Db  665 TAGTCCCGTTTTCCTTACTTGGGGCCCAAGGACTCTGGTCACTGCTCT 711

RESULT 5
US-08-224-591-17
; Sequence 17, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
```

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,845  
FILING DATE: 15-JAN-1993  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 733 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..723)  
US-08-224-591-17

Query Match 73.3%; Score 257.4; DB 2; Length 733;  
Best Local Similarity 83.9%; Pred. No. 4.8e-77;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGAGCTGTGGAGTCTGGGGAGGGGTTGTGCGAGCTCGAAGGTCCTTGAGACTCT 61  
DB 377 AAGTGAAGCTTGTGGAGTCTGGGGAGGGGTTGTGAAAGCTCGCTGAAACTCT 436

QY 62 CTTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121  
DB 437 CTTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 496

QY 122 CGGCAAGGGTCTGGAGTGGGTGCGAAAAGTTAGTAGTGGTGGTGTAGTACCTACTATT 181  
DB 497 CGGCAAGGGTCTGGAGTGGGTGCGAACCACTTAGTAGTGGTGTAGTACCTACTATT 556

QY 182 TAGACACTGTGAGGCGGCGATTCACCATCTCCAGAGACAAATAGTAGTAAAGACCACTATACC 241  
DB 557 TAGACAGTGTGAAGGCGGCGATTCACCATCTCCAGAGACAGTCCAGGAAACACCTTATACC 616

QY 242 TCGAAATGAACCTCTCTGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATACT 301  
DB 617 TCGAAATGAGAGCTGTGAGGCTGTGAGGACACGCGCTTGTATTACTGTGCGCCGACTACGG 676

QY 302 ACGGCAAGTTTCTTACTTGGGCGCAAGGAGCTACAGTGTGCTTCT 348  
DB 677 TAGTCCCGTTTCTTACTTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 723

RESULT 6  
US-08-791-391-17  
Sequence 17, Application US/08926789  
Patent No. 5990275  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/926,789  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/224,591  
FILING DATE:  
APPLICATION NUMBER: US 08/002,845  
FILING DATE: 15-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/980,529  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 733 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..723)  
US-08-926-789-17

Query Match 73.3%; Score 257.4; DB 2; Length 733;  
Best Local Similarity 83.9%; Pred. No. 4.8e-77;  
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGAGCTGTGGAGTCTGGGGAGGGGTTGTGCGAGCTCGAAGGTCCTTGAGACTCT 61  
DB 377 AAGTGAAGCTTGTGGAGTCTGGGGAGGGGTTGTGAAAGCTCGCTGAAACTCT 436

QY 62 CTTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 121  
DB 437 CTTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGGCTC 496

QY 122 CGGCAAGGGTCTGGAGTGGGTGCGAAAAGTTAGTAGTGGTGGTGTAGTACCTACTATT 181  
DB 497 CGGCAAGGGTCTGGAGTGGGTGCGAACCACTTAGTAGTGGTGTAGTACCTACTATT 556

QY 182 TAGACACTGTGAGGCGGCGATTCACCATCTCCAGAGACAAATAGTAGTAAAGACCACTATACC 241  
DB 557 TAGACAGTGTGAAGGCGGCGATTCACCATCTCCAGAGACAGTCCAGGAAACACCTTATACC 616

QY 242 TCGAAATGAACCTCTCTGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATACT 301  
DB 617 TCGAAATGAGAGCTGTGAGGCTGTGAGGACACGCGCTTGTATTACTGTGCGCCGACTACGG 676

QY 302 ACGGCAAGTTTCTTACTTGGGCGCAAGGAGCTACAGTGTGCTTCT 348  
DB 677 TAGTCCCGTTTCTTACTTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 723

RESULT 7  
US-08-579-378A-19  
Sequence 19, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: L-Selectin  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheutz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405

us-08-579-378A-19

Query Match 70.3%; Score 246.8; DB 4; Length 405;  
Best Local Similarity 84.1%; Pred. No. 1.3e-73;  
Matches 291; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTCCAGCCCTGGAGGTCCTCGAGACTCT 61  
DB 59 AAGTGCAACTGGTGGAGTCTGGGGAGGCGTTAGTCAGCCCTGGAGGAGCTTGAGACTCT 118  
QY 62 CCGTGCAGCCCTCGGATTCACCTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 121  
DB 119 CCGTGCAGCCCTCGGATTCACCTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 178  
QY 122 CGGGAAGGGTCTGGAGTGGGTTCGCAAAAGTTAGTAGTGGGTGGTAGCACCCTACTATT 181  
DB 179 CAGGGAAGGGACTCGAGTGGGTTCGCAATCCATTAGTA---CTGGTGGTAGCACCCTACTATC 235  
QY 182 TAGACACTGTCAGGCGCGGATTCACCTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 241  
DB 236 CAGACAGTGTGAAGGCGCGGATTCACCTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 295  
QY 242 TCGAAATGAACCTCTCGAGAGCCGAGACAGCCGCTGTTACTGTGCAAGACATAACT 301  
DB 296 TCGAATGAATCTCTGAGGCTGAGGACAGCCGCTGTTACTGTGCAAGACATAACT 347  
QY 302 ACGGCAGTTTCTGCTTACTGGGGCCCAAGGACTACAGTGAAGTCTGTTTC 347

DB 356 ACGGCTATTTTGACTACTGGGGCCCAAGGCAACCCCTGGTGCACAGTCTC 401

# RESULT

PCT-US96-13152-3

; Sequence 3, Application PC/TUS9613152  
; GENERAL INFORMATION:

; APPLICANT: Martin, Ulrich, et al.  
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch  
; ADDRESSEE: Attn: Norman D. Hanson  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/13152

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: 27-Dec-95

APPLICATION NUMBER: EP 95 112 895.8

FILING DATE: 17-Aug-95

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:

NAME: Norman D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PPE/NDH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1329 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1329

FEATURE:

NAME/KEY: mat\_peptide

LOCATION: 1

PCT-US96-13152-3

Query Match 70.3%; Score 246.8; DB 5; Length 1329;  
Best Local Similarity 84.1%; Pred. No. 2.3e-73;  
Matches 291; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCGTTGTCCAGCCCTGGAGGTCCTCGAGACTCT 61

DB 2 AAGTGCAACTGGTGGAGTCTGGGGAGGCGTTAGTCAGCCCTGGAGGAGCTTGAGACTCT 61

QY 62 CCGTGCAGCCCTCGGATTCACCTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 121

DB 62 CCGTGCAGCCCTCGGATTCACCTTCAGTAGCTATGACATGCTCTTGGGTTCGCCAGGCTC 121

QY 122 CGGGAAGGGTCTGGAGTGGGTTCGCAAAAGTTAGTAGTGGGTGGTAGCACCCTACTATT 181

DB 122 CAGGGAAGGGACTCGAGTGGGTTCGCAATCCATTAGTA---CTGGTGGTAGCACCCTACTATC 178

179	Db	179	CAGAGAGAGCGTGGAGTGGGTGCGAGAAATTAGTGGTGGTAATTACGCCCTACTATC	238
182	Qy	182	TAGACACTGTGCAGGGCCGATTACCATCTCCAGAGACAAATAGTAGAGACACCCCTATACC	241
239	Db	239	AAGACACTGTGAGGGCCGATTACCATCTCCAGAGACAAATGCCAAGAACACCCCTGTACC	298
242	Qy	242	TGCAAAATGAACCTCTCAGAGCGCGAGGACACACCGCTGTATTACTGTGCAAGACATAACT	301
299	Db	299	TGGAATATGACAGTCTGAGTCTGAGGACACGGCCATGTATTACTGTGCAAGGAGGACT	358
302	Qy	302	ACGG-----CAGTTTTCCTTACTGGGGCCAAAGGGACTACAGTCACTGTTCT	348
359	Db	359	ACGATATCCGGGCGCTGGTTTGGCTTACTGGGGCCAAAGGACTCTGGTCTGTGCTCT	414

RESULT 10  
 US-08-129-930B-27  
 ; Sequence 27, Application US/08129930B  
 ; Patent No. 5804187  
 ; GENERAL INFORMATION:  
 ; APPLICANT: do Couto Dr., Fernando J.R.  
 ; APPLICANT: Ceriani Dr., Roberto L.  
 ; APPLICANT: Peterson Dr., Jerry A.  
 ; APPLICANT: Padlan Dr., Eduardo A.  
 ; TITLE OF INVENTION: Analogue Peptides With Broad  
 ; TITLE OF INVENTION: Carcinoma Specificity, and kit and  
 ; TITLE OF INVENTION: Diagnostic Vaccination and  
 ; TITLE OF INVENTION: Therapeutic Methods  
 ; NUMBER OF SEQUENCES: 96  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: V. AMZEL & ASSOC.  
 ; STREET: 2055 No. 5804187th Broadway, Suite 201  
 ; CITY: Walnut Creek  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94596  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/129,930B  
 ; FILING DATE: September 30, 1993  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Amzel Ph.D., Viviana  
 ; REGISTRATION NUMBER: 30,930  
 ; REFERENCE/DOCKET NUMBER: CRFCC-008A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (510) 521-1333  
 ; TELEFAX: (510) 521-3541  
 ; TELEX: n.a.  
 ; INFORMATION FOR SEQ ID NO: 27:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 418 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 US-08-129-930B-27

Query Match 69.7%; Score 244.8; DB 1; Length 418;  
Best Local Similarity 82.9%; Pred. No. 6.3e-73;  
Matches 295; Conservative 0; Mismatches 52; Indels 9; Gaps

QY	2	AGGTGCAGCTGGTGGACTCGGGGAGGCGTTGTGACGCTGGAAGGTCCCTCAGACTCT	61
Db	59	AAGTGCAAGATGGTGGACTTCGGGGAGGCTTAGTGAAGCTGGAGGTCCTCGAAACTCT	118
QY	62	CTGTGACAGCCTCTGGATTCACTTCAGTAGCTATGACATGTCTTCGGTTCGCCAGGCWC	121

Db 119 CCGTGCAGCCTCTCGATTGCGTTTTCAGTAGCTATGCCATGCTCTGGGTTGCCAGCTCTC 178  
QY 122 CGGGCAAGGCTGTGAGTGGGTCGCAAAAGTTAGTAGTGGTGTAGCAGCCTACTATT 181  
Db 179 CAGAGAAGGCTGGAGTGGGTCGAGAAATTTAGTAGTGGTAAATACGCCCTACTATC 238  
QY 182 TAGACACTGTGAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
Db 239 AAGACACTGTGAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 298  
QY 242 TGCRAATGAACCTCTGTAGAGCCGAGGACAGACCGCTGTATTACTGTGCAAGACATAACT 301  
Db 299 TGGAAATGAGCAGTCTGAGTGTGAGTGTGAGGCGCGCATGTATTACTGTGCAAGGAGGACT 358  
QY 302 ACGG-----CAGTTTTCCTACTGGGCGCAAGGACTACACTGACTGTTCT 348  
Db 359 ACGGTATCCCGGCGTGGTTTGTCTACTGGGCGCAAGGACTGTGCTCTCTGTCTCT 414

## RESULT 11

US-08-672-176A-3  
; Sequence 3, Application US/08672176A  
; Patent No. 5908925  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Margo P.; Shearman, Clyde W.  
; TITLE OF INVENTION: Genetically Engineered Immunoglobulins with  
; TITLE OF INVENTION: Specificity for Glycated Albumin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Exocell, Inc.  
; STREET: 3508 Market Street, suite 420  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage  
; COMPUTER: PC  
; OPERATING SYSTEM: DOS 4.0 or better  
; SOFTWARE: Wordperfect, Version 5.2  
; CURRENT APPLICATION DATA: US/08/672.176A  
; APPLICATION NUMBER: unknown  
; FILING DATE: unknown  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: N/A  
; FILING DATE: N/A  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silver, Robert S.  
; REGISTRATION NUMBER: unknown  
; REFERENCE/DOCKET NUMBER: E1042/20002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-567-2010  
; TELEFAX: 215-751-1142  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 base pairs/120 amino acid residues  
; TYPE: nucleic acid/amino acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: humanized A17 heavy chain variable region  
; HYPOTHETICAL: yes  
; ANTI-SENSE: no  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE: synthetic  
; ORGANISM: N/A  
; STRAIN: N/A  
; INDIVIDUAL ISOLATE: N/A  
; DEVELOPMENTAL STAGE: N/A  
; HAPLOTYPE: N/A  
; TISSUE TYPE: N/A

CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: plasmid  
LIBRARY: N/A  
CLONE: pHuA717VH-1  
POSITION IN GENOME: N/A  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS: human framework regions; murine CDRs  
NAME/KEY: FR-1; CDR-1; FR-2; CDR-2; FR-3; CDR-3; FR-4  
LOCATION: aa#1-30; aa#31-35; aa#36-49; aa#50-66;  
LOCATION: aa#67-98; aa#99-109; aa#110-120  
IDENTIFICATION METHOD: similarity to known sequences  
OTHER INFORMATION: antigen is human glycated albumin  
PUBLICATION INFORMATION: N/A  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 3:  
US-08-672-176A-3  
  
Query Match 68.5%; Score 240.6; DB 2: Length 360;  
Best Local Similarity 82.3%; Pred No. 1.5e-71;  
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;  
  
QY 2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTGCAGCCTGGAAAGGTCCTTGAGACTCT 61  
Db 2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGTGCAGCCTGGAAAGGTCCTTGAGACTCT 61  
QY 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTCTGGTGGTCCGAGGCTC 121  
Db 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTCTGGTGGTCCGAGGCTC 121  
QY 122 CGGGCAAGGCTGTGAGTGGGTCGCAAAAGTTAGTAGTGGTGTAGCAGCCTACTATT 181  
Db 122 CTGGCAAGGCTGTGAGTGGGTCGCAAAAGTTAGTAGTGGTGTAGCAGCCTACTATT 181  
QY 182 TAGACACTGTGAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241  
Db 182 CAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCGTTGTACC 241  
QY 242 TGCRAATGAACCTCTGTGAGAGCCGAGGACAGACCGCTGTATTACTGTGCAAGA----- 294  
Db 242 TGCRAATGAACCTCTGTGAGAGCCGAGGACAGACCGCTGTATTACTGTGCAAGAGATGTT 301  
QY 295 --CATAACTACGGCAGTCTTGTCTTACTGGGCGCAAGGACTACAGTGTGTTTC 347  
Db 302 ATCTTTTACTATCTATCTGACTACTGGGCTCAAGGACCAACACAGTCAACCGTCTC 356

## RESULT 12

US-08-672-176A-5  
; Sequence 5, Application US/08672176A  
; Patent No. 5908925  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Margo P.; Shearman, Clyde W.  
; TITLE OF INVENTION: Genetically Engineered Immunoglobulins with  
; TITLE OF INVENTION: Specificity for Glycated Albumin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Exocell, Inc.  
; STREET: 3508 Market Street, suite 420  
; CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage  
COMPUTER: PC  
OPERATING SYSTEM: DOS 4.0 or better  
SOFTWARE: Wordperfect, Version 5.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,176A  
FILING DATE: unknown  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: N/A  
FILING DATE: N/A  
ATTORNEY/AGENT INFORMATION:  
NAME: Silver, Robert S.  
REGISTRATION NUMBER: unknown  
REFERENCE/DOCKET NUMBER: E1042/20002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-567-2010  
TELEFAX: 215-751-1142  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 720 base pairs/240 amino acid residues  
TYPE: nucleic acid/amino acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: humanized A17 immunoglobulin single-chain Fv  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
FRAGMENT TYPE: N-terminal fragment  
ORIGINAL SOURCE: synthetic  
ORGANISM: N/A  
STRAIN: N/A  
INDIVIDUAL ISOLATE: N/A  
DEVELOPMENTAL STAGE: N/A  
HAPLOTYPE: N/A  
TISSUE TYPE: N/A  
CELL TYPE: N/A  
CELL LINE: N/A  
ORGANELLE: N/A  
IMMEDIATE SOURCE: plasmid  
LIBRARY: N/A  
CLONE: pHuA17ScFv-1  
POSITION IN GENOME: N/A  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE: HuA17VH-1 linked to HuA17VL  
NAME/KEY: HuA17VH; linker: HuA17VL  
LOCATION: aa# 1-120; aa# 121-133; aa# 134-240  
IDENTIFICATION METHOD: similarity to known sequences  
OTHER INFORMATION: antigen is human glycosylated albumin  
PUBLICATION INFORMATION: N/A  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 5:  
US-08-672-176A-5

Query Match 68.5%; Score 240.6; DB 2; Length 720;  
Best Local Similarity 82.3%; Pred. No. 2.1e-71;  
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTGGAAGGTCCTCGAGACTCT 61  
DB 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCTGGAAGGTCCTCGAGACTCT 61  
QY 62 CTTGTGCAGCCCTCTGGATTACCTTCAGTAGCTATGACATGTCTTGGTTCGCGAGGTC 121  
DB 62 CTTGTGCAGCCCTCTGGATTACCTTCAGTAGCTATGACATGTCTTGGTTCGCGAGGTC 121  
QY 122 CGGGCAAGGTCGTGGAGTGGTGGCAAAAGTTAGTAGTGTGTGCTAGCAGCTACTATT 181  
DB 122 CGGGCAAGGTCGTGGAGTGGTGGCAAAAGTTAGTAGTGTGTGCTAGCAGCTACTATT 181  
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAAATAGTAAGACACCTTATAC 241  
DB 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAAATAGTAAGACACCTTATAC 241  
QY 242 TGAATGAATGAACTCTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGA----- 294  
DB 242 TGAATGAATGAACTCTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGAAGATGGT 301  
QY 295 --CATAACTACGCGAGTTTGTCTTACTGGGCGCAAGGACTACAGTGACTGTTC 347  
DB 302 ATCTTTATTACTATGCTATGGACTACTGGGTCAAGGAACACAGTACCGTCTC 356  
RESULT 13  
US-08-475-000-15  
; Sequence 15, Application US/08475000  
; Patent No. 5811267  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,000  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..357  
US-08-475-000-15

Query Match 68.3%; Score 239.8; DB 1; Length 357;  
Best Local Similarity 82.2%; Pred. No. 2.8e-71;  
Matches 290; Conservative 0; Mismatches 57; Indels 6; Gaps 1;



```
QY      2 AGTGCAGCTGTGGAGTCTGGGGAGGGCTGTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2 AGTGAAGGTTGTGGAGTCTGGGGAGTCTTAGTGAGGCTGGAGGGTCCCTGAAACTCT 61
QY      62 CCTGTCCAGCCTCTGGATTTCACCTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGGCTC 121
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 CCTGTCCAGCCTCTGGATTTCACCTTCAGTAGGTATACCATGTCTTGGGTTCGCCAGACTC 121
QY      122 CGGGCAAGGCTCTGGAGTGGGTCCGCAAAAGTTAGTAGTGGTGGTGTAGCACCTACTATT 181
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
122 CGGAGAAGCGGCTGGAGTGGGTCCGAACCATTTAGTAGTGGTGGTGTAAACCTACTATC 181
QY      182 TAGACACTGTGCAGGCCCGATTCCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
182 CAGACAGTGTGAAGGTCGATTCCACCGTCTCCAGAGACAATGCCATGAGCAGCCTGTACC 241
QY      242 TGCAAATGAACCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACA----- 296
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
242 TGCAAATGAGCAGCTCTGAGGTCTGAGGACACAGCCCTTGTATTACTGTGCAAGATACGGGG 301
QY      297 -TAACTACGGCAGTTTGTCTTACTGGGGCCAGGGACTACAGTGACTGTTTCT 348
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
302 CTGGTGACCGCTGGTTGTCTTACTGGGGCCAGGGACTCTGGTFCACAGTTTCT 354
```

Search completed: October 11, 2001, 15:14:12  
Job time: 4999 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 11:57:35 ; Search time 31.63 seconds  
(without alignments)  
281.771 Million cell updates/sec

Title: US-08-791-391A-2

Perfect score: 616

Sequence: 1 QVQLVESGGGVVQPGKSLRL.....RHNYGSFAYWGQGTIVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	507	82.3	119	2 S31108	Ig heavy chain - h
2	503	81.7	119	2 C36005	Ig heavy chain v r
3	503	81.7	119	2 S31107	Ig heavy chain - h
4	503	81.7	121	2 S19666	Ig heavy chain v r
5	503	81.7	127	2 S38489	Ig heavy chain - h
6	503	81.7	140	2 S31588	Ig heavy chain v r
7	502	81.5	140	2 S31586	Ig heavy chain v r
8	501	81.3	134	2 S31679	Ig heavy chain v r
9	500.5	81.2	122	2 E36005	Ig heavy chain v r
10	499	81.0	132	2 S31603	Ig heavy chain v r
11	498.5	80.9	122	2 S31117	Ig heavy chain - h
12	498.5	80.9	128	2 S48797	Ig heavy chain v r
13	498	80.8	121	2 G36005	Ig heavy chain v r
14	494	80.2	119	2 D36005	Ig heavy chain v r
15	494	80.2	119	2 F36005	Ig heavy chain v r
16	494	80.2	123	2 S31114	Ig heavy chain - h
17	494	80.2	138	2 S31666	Ig heavy chain v r
18	493.5	80.1	120	2 S48798	Ig heavy chain v r
19	492.5	80.0	114	2 S46392	Ig heavy chain v r
20	492	79.9	117	2 S78486	Ig heavy chain v r
21	492	79.9	160	2 S05271	Ig heavy chain pre
22	491.5	79.8	114	2 S46390	Ig heavy chain v r
23	490	79.5	131	2 I55673	Ig heavy chain - h
24	488.5	79.3	137	2 S31701	Ig heavy chain v r
25	487	79.1	134	2 S31699	Ig heavy chain v r
26	485.5	78.8	118	2 S31116	Ig heavy chain - h
27	485.5	78.8	140	2 S70442	Ig heavy chain pre
28	485	78.7	133	2 A49028	Ig heavy chain v r
29	485	78.7	143	2 S23624	Ig heavy chain v r

ALIGNMENTS

RESULT 1

S31108

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C:Accession: S31108

R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp

A:Reference number: S31104; MUID:92111633

A:Accession: S31108

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-119 <RAA>

A:Cross-references: EMBL:X62956

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 507; DB 2; Length 119;  
Best Local Similarity 82.4%; Pred. No. 2e-39;  
Matches 98; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDSMWVRQAPGKGLVWVAKVSSGGSTYY 60

Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVVRQAPGKGLVWVSAITSGGGSTYY 60

Qy 61 LDTVGRTTISRDNSKNTLYLQMNSLRAEDTAVYCA--RHNYGSFAYWGQGTIVTVSS 117

Db 61 ADSVKGRTTISRDNSKNTLYLQMNSLRAEDTAVYCAKDRRLTGTFYWGQGTIVTVSS 119

RESULT 2

C36005

Ig heavy chain v region (30p1) - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Aug-1996

C:Accession: C36005

R:Schröder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge

A:Reference number: A36005; MUID:90349571

A:Accession: C36005

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SCH>

A:Cross-references: GB:M18513

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

```
Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.5e-39;
Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVAISGSGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LPTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAH-NYGS-FAYWGQTTVTSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVAGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDGAGSGFDYWGQGLTVTSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Ragaporst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62955
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 4.5e-39;
Matches 98; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVAISGSGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LPTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAHNYGS--FAYWGQTTVTSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVAGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDPGASYYFDYWGQGLTVTSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MA>
A:Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 4.6e-39;
Matches 98; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWAKVSSGGSTYY 60
```

```
Db 1 QVQLVQSGGGVVPQGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVSDGSNKYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LPTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAHNY----GSFAYWGQTTVTYS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVAGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKTYSGSGWGYFDYWGQGLTVTYS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 S 117
Db 121 S 121

RESULT 5
S38489
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z23028; NID:g414025; PIDN:CAA80563.1; PID:g414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 127;
Best Local Similarity 77.2%; Pred. No. 4.8e-39;
Matches 98; Conservative 6; Mismatches 11; Indels 12; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGGGVVPQGRSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVAISGSGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LPTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAH-----NYGSFAYWG 108
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVAGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKEGPPASDYDSSGYYSFDYWG 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 109 QGTTVT 115
Db 121 QGTLTV 127

RESULT 6
S31588
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31588
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CU>
A:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 140;
Best Local Similarity 80.2%; Pred. No. 5.4e-39;
Matches 97; Conservative 11; Mismatches 9; Indels 4; Gaps 2;
```

[illegible]

RESULT 7

S31686

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31686

R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Accession: S31686

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-140 <GUI>

A/Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

RESULT 8

S31679

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31679

R:Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A:Submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31679

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-134 <CDU>

A:Cross-references: EMBL: Z14203; NID: g30965; PID: CAA78572.1; PID: g30966

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Qy	1	QQVLVESGGGVVQGRSLURLSCAASGFTFSYDSMSWVRQAPEGKLEWVAKVSSGGGSTYY	60
Db	20	QQVLVESGGGVVQGRSLURLSCAASGFTFSYAHHWVRQAPEGKLEWVAVISDGSNKY	79
Qy	61	LDTVQGRTISRDNSKNLYLQMNSLRADTAIVYCARRHNYGSFAYWGQTITVTSS	117
Db	80	ADSVKGRTISRDNKNTLYLQMNSLRADTAIVYCARESGD-YWGQGLTITVTSS	134
RESULT                 9			
E36005			
Ig heavy chain V region (M7) - human			
C:	Species:	Homo sapiens (man)	
C:	Date:	21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998	
C:	Accession:	E36005	
R:	Schroeder Jr., H.W.; Wang, J.Y.		
A:	Title:	Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990	
A:	Reference number:	A36005; MUID:90349571	
A:	Status:	preliminary	
A:	Molecule type:	mRNA	
A:	Residues:	1-122 <SCH>	
A:	Cross-references:	GB:M34030	
C:	Genetics:		
A:	Gene:	GDB:IGH@: IGHDI1	
A:	Cross-references:	GDB:I18731; OMIM:146910	
A:	Map position:	Iq32.33-Iq32.33	
C:	Superfamily:	immunoglobulin v region; immunoglobulin homology	
C:	Keywords:	heterotetramer; immunoglobulin	
F:	15-98/Domain:	immunoglobulin homology <IMM>	

```

RESULT 10
S31603
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31603
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from
A:Reference number: S31585
A:Accession: S31603
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-113/Domain: immunoglobulin homology <IMM>

```

```

F:15-98/Domain: immunoglobulin homology <IMM>

      Query Match      80.9%;   Score 498.5;   DB 2;   Length 128;
      Best Local Similarity 78.1%;   Pred. No. 1.3e-38;
      Matches 100; Conservative 5; Mismatches 12; Indels 11; Gaps 2;

QY 1 QVQLVESGGGVQPGRSLRLSCAASGFTFSYDMSWYRQAPGKGLEWAKVSSGGSTYY 60
Db 1 QVQLVESGGGVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWAVIWTYDGSNKYY 60

QY 61 LDTVQGRFTISRNSKNTLYLQWNSLRAEDTAVYYCARHNY-----GSFAY-----WGQ 109
Db 61 ADSVKGRFTISRNSKNTLYLQWNSLRAEDTAVYYCARDNYYYDSSYYYYYYGMDVWGQ 120

QY 110 GTTIVTVSS 117
Db 121 GTTIVTVSS 128

RESULT 13
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005;MUID:90349571

```

```

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: GB:M34031
C:Genetics:
A:Gene: GDB:ICHE: IGHDIY1
A:Cross-references: GDB:118731; OMIM:145910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      80.8%; Score 498; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. NO. 1.3e-38;
Matches 98; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Qy    1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYDSMWVRQAPGKGLEWVAKVSSGGSTYY 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : | : ||
Db    1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYAHNWVRQAPGKGLEWVAIVSYDGSNKYY 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : | : |||

Qy    61 LDTVQRFTISRNSKNNTLYLQNLSRAEDTAVYYCARH----NYGSFAYWGOGTTVTVS 116
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : | : ||||| ||||
Db    61 ADSVKGRFTISRNSKNNTLYLQNLSRAEDTAVYYCARORKDWGWFALFDYWGGTLVTVS 120
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : | : ||||| ||||

Qy    117 S 117
      |
Db    121 S 121

RESULT .14
D36005
Ig heavy chain V region (M43) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: D36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571
A:Accession: D36005
A>Status: preliminary

```

A:Molecule type: mRNA  
A:Residues: 1-119 <SCH>  
A:Cross-references: GB:M34024  
C:Genetics:  
A:Gene: GDB:IGH@; IGHDI  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 494; DB 2; Length 119;  
Best Local Similarity 79.8%; Pred. No. 3e-38;  
Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVQPCRSRLSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRAEDTAVYYCARHNYGS--FAYWGOGTTVTYSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKKNWDFDPWGOGTTVTYSS 119  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15  
F36005  
Ig heavy chain V region (M49) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence,revision 21-Dec-1990 #text\_change 16-Dec-1998  
C:Accession: F36005  
R:Schroeder Jr., H.W.; Wang, J.Y.  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A36005; MUID:90349571  
A:Accession: F36005  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <SCH>  
A:Cross-references: GB:M34026  
C:Genetics:  
A:Gene: GDB:IGH@; IGHDI  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 494; DB 2; Length 119;  
Best Local Similarity 82.4%; Pred. No. 3e-38;  
Matches 98; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVQPCRSRLSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 QVQLVESGGGVQPCRSRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISYDGSNKYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRAEDTAVYYCARHNYGSFAY--WGOGTTVTYSS 117  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDKASDAFDIWGOGTTVTYSS 119  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: October 11, 2001, 12:02:35  
Job time: 300 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:02:00 ; Search time 17.83 Seconds  
(without alignments)  
224.784 Million cell updates/sec

Title: US-08-791-391A-2

Perfect score: 616

Sequence: 1 QVQLVESGGGVQPGKSLRL.....RHNYGSFAYWGQGTITVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	481.5	78.2	122	1 HV3G_HUMAN	P01768 homo sapien
2	456	74.0	121	1 HV3J_HUMAN	P01771 homo sapien
3	453	73.5	119	1 HV3I_HUMAN	P01770 homo sapien
4	451.5	73.3	136	1 HV16_MOUSE	P01783 mus musculus
5	449.5	73.0	126	1 HV3K_HUMAN	P01772 homo sapien
6	446	72.4	117	1 HV3C_HUMAN	P01764 homo sapien
7	442.5	71.8	114	1 HV3B_HUMAN	P01763 homo sapien
8	441.5	71.7	116	1 HV3T_HUMAN	P01781 homo sapien
9	441.5	71.7	122	1 HV3H_HUMAN	P01769 homo sapien
10	428	69.5	117	1 HV55_MOUSE	P18526 mus musculus
11	424	68.8	115	1 HV3F_HUMAN	P01767 homo sapien
12	423	68.7	119	1 HV3L_HUMAN	P01773 homo sapien
13	418.5	67.9	116	1 HV05_CARAU	P19181 carassius a
14	418	67.9	117	1 HV54_MOUSE	P18525 mus musculus
15	415.5	67.5	119	1 HV37_MOUSE	P01807 mus musculus
16	415.5	67.5	119	1 HV40_MOUSE	P01810 mus musculus
17	415	67.4	115	1 HV3D_HUMAN	P01765 homo sapien
18	415	67.4	120	1 HV3E_HUMAN	P01766 homo sapien
19	410.5	66.6	119	1 HV3M_HUMAN	P01774 homo sapien
20	408.5	66.3	119	1 HV3N_HUMAN	P01775 homo sapien
21	407.5	66.2	120	1 HV3U_HUMAN	P01782 homo sapien
22	407.5	66.2	122	1 HV3A_HUMAN	P01762 homo sapien
23	406	65.9	117	1 HV02_CANFA	P01785 canis fami
24	405.5	65.8	114	1 HV01_CANFA	P01784 canis fami
25	404	65.6	115	1 HV32_MOUSE	P01801 mus musculus
26	403.5	65.5	119	1 HV38_MOUSE	P01808 mus musculus
27	402.5	65.3	122	1 HV20_MOUSE	P01789 mus musculus
28	402	65.3	113	1 HV30_MOUSE	P01799 mus musculus
29	400	64.9	142	1 HV01_RAT	P01805 rattus norv
30	399	64.8	118	1 HV39_MOUSE	P01809 mus musculus
31	397	64.4	113	1 HV27_MOUSE	P01796 mus musculus
32	395.5	64.4	97	1 HV56_MOUSE	P18527 mus musculus
33	395.5	64.2	111	1 HV35_MOUSE	P01804 mus musculus

#### ALIGNMENTS

##### RESULT 1

```

HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RL location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

```

Query Match 78.2%; Score 481.5; DB 1; Length 122;  
Best Local Similarity 74.6%; Pred. No. 9.9e-42;  
Matches 91; Conservative 12; Mismatches 14; Indels 5; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNWVRQAPGKGLWYAKVSSGGSTYY 60

Db 1 QVELVESGGGVVZPGKSLRLSCAASGFTFSNYAMHWVRQPPGKGLWYAVTSYGBBKYY 60

Qy 61 LDTVGGRFTISRDNKNLYLQMNLSRAEDTAVYYCARH-----NYGSFAYWGQGTITV 115

Db 61 ABSVKGRTISRDSKBTLYLQMNLSRAETAVYYCARDPLRYGFRFNYWGQGTITV 120

Qy 116 SS 117

Db 121 SS 122

##### RESULT 2

HV3J\_HUMAN

ID HV3J\_HUMAN STANDARD; PRT; 121 AA.

AC P01771;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V-III REGION HIL.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79124695; PubMed=420800;  
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;  
 RT "Amino acid sequence of the VH region of human myeloma  
 cryoglobulin IgG H1L";  
 RL Biochemistry 18:553-560(1979).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 DR PIR; A02054; GIHULH.  
 DR HSSP; P01772; 2IG2.  
 DR InterPro: IPR003006;  
 DR Pfam; PF00047; Ig; 1.  
 DR MOD\_RES 1 1  
 KW Immunoglobulin V region.  
 FT DISULFID 22 96  
 FT NON\_TER 119 119  
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 74.0%; Score 456; DB 1; Length 121;  
 Best Local Similarity 73.6%; Pred. No. 3.6e-39;  
 Matches 89; Conservative 9; Mismatches 19; Indels 4; Gaps 1;  
 QY 1 QVQLVSGGVPQGRSLRSLCAASGFTSSYDMVSRQAPGKGLWAKVSSGGSTYY 60  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 QVQLVAGGVPQGRSLRSLCAASGFTSSYDMVSRQAPGKGLWAVIWTNGSRITY 60  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 LDTVQGRFTISRDNKNTLYLNMSLRADETAVYYCARH----NYGSFAYWGQGTVTVS 116  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 GDSVKGRTISRDNKNTLYLNMSLRADETAVYYCARDPDILTAISFDYWGQGLVTVS 120  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 117 S 117  
 DB 121 S 121

RESULT 3  
 HV31\_HUMAN STANDARD; PRT; 119 AA.  
 AC P01770;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V-III REGION NIE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77070269; PubMed=826475;  
 RA Ponstingl H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a  
 monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The  
 chymotryptic peptides of the H-chain, alignment of the tryptic  
 peptides and discussion of the complete structure."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 IgG1 immunoglobulin (myeloma protein NIE). I: Purification and  
 characterization of the protein, the L- and H-chains, the  
 cyanogen bromide cleavage products, and the disulfide bridges."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 PIR; A02053; GIHUNI.

DR HSSP; P01772; 2IG2.  
 DR InterPro: IPR003006;  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT MOD\_RES 1 1  
 FT DISULFID 22 96  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;

Query Match 73.5%; Score 453; DB 1; Length 119;  
 Best Local Similarity 75.6%; Pred. No. 7e-39;  
 Matches 90; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVSGGVPQGRSLRSLCAASGFTSSYDMVSRQAPGKGLWAKVSSGGSTYY 60  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 QVQLVSGGVPQGRSLRSLCAASGFTSSYDMVSRQAPGKGLWAVMSYBGBKH 60  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 LDTVQGRFTISRDNKNTLYLNMSLRADETAVYYCARHNYGS--FAYWGQGTVTVS 117  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 ADSVNGRTISRDNKNTLYLNMSLRADETAVYYCARIRDTAMFFAHWGQGLVTVS 119  
 I:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4  
 HV16\_MOUSE STANDARD; PRT; 136 AA.  
 AC P01783;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPb family of  
 antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 RN [2]  
 RP SEQUENCE OF 17-136.  
 RX MEDLINE=77100368; PubMed=401950;  
 RA Adetugbo K., Milstein C., Secher D.S.;  
 RT "Molecular analysis of spontaneous somatic mutants."  
 RL Nature 265:299-304(1977).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J00522; AAD15290.1;  
 DR PIR; A02066; GMS21.  
 DR InterPro: IPR003006;  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 16  
 FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.  
 FT DOMAIN 115 119 D SEGMENT.  
 FT DOMAIN 120 136 JH4 SEGMENT.  
 FT DISULFID 38 112  
 FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).  
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).  
 FT CONFLICT 115 115 W -> H (IN REF. 2).  
 FT CONFLICT 120 120 Y -> W (IN REF. 2).



FT NON\_TER 136 136  
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 73.3%; Score 451.5; DB 1; Length 136;  
Best Local Similarity 74.8%; Pred. No. 1.1e-38;  
Matches 89; Conservative 12; Mismatches 15; Indels 3; Gaps 2;

QY 2 VOLVESGGVQPGSRSLRLSCAASGFTFSYDMWVRQAPGKLEWAKVSSGGSTYYL 61  
DB 18 VOLVESGGGLVQPGSRSLRLSCAASGFTFSYDMWVRQAPGKLEWAKVSSGGSTLHYA 77  
QY 62 DTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQSTTVTVSS 117  
DB 78 DTVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQSTTVTVSS 136

RESULT 5  
HV3K\_HUMAN STANDARD; PRT; 126 AA.  
AC P01772;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V-III REGION KOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE, AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.,  
RT "Three-dimensional structure determination of antibodies. Primary  
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.,"  
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
[2]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE=81072295; PubMed=7441755;  
RA Marquart M., Delsenhofer J., Huber R., Palm W.,  
RT "Crystallographic refinement and atomic models of the intact  
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A  
RT and 1.0-A resolution."  
RJ J. Mol. Biol. 141:369-391(1980).  
DR PIR: A02055; GIHUKL.  
DR PDB: 2FB4; 12-JUL-89.  
DR PDB: 2IG2; 12-JUL-89.  
DR InterPro: IPR003006; -.  
DR Pfam: PF00047; Ig; 1.  
KW Immunoglobulin V region; 3D-structure.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 96  
FT DISULFID 105 110  
FT STRAND 3 7  
FT STRAND 11 12  
FT TURN 14 15  
FT STRAND 18 25  
FT HELIX 29 31  
FT STRAND 34 39  
FT TURN 41 42  
FT STRAND 46 51  
FT TURN 53 54  
FT STRAND 58 60  
FT TURN 62 67  
FT STRAND 68 73  
FT TURN 74 77  
FT STRAND 78 83  
FT HELIX 88 90  
FT STRAND 92 99  
FT STRAND 106 106  
FT TURN 107 108  
FT STRAND 109 109  
FT STRAND 113 113

FT STRAND 120 124  
FT NON\_TER 126 126  
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 73.0%; Score 449.5; DB 1; Length 126;  
Best Local Similarity 71.4%; Pred. No. 1.7e-38;  
Matches 90; Conservative 10; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVOLVESGGVQPGSRSLRLSCAASGFTFSYDMWVRQAPGKLEWAKVSSGGSTYY 60  
DB 1 QVOLVESGGVQPGSRSLRLSCAASGFTFSYDMWVRQAPGKLEWAKVSSGGSTYY 60  
QY 61 LDTVOGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQST 111  
DB 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAR--HNYGSFA--YWGQST 120

QY 112 TVTVSS 117  
DB 121 PTVTVSS 126

RESULT 6  
HV3C\_HUMAN STANDARD; PRT; 117 AA.  
AC P01764;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81101090; PubMed=6450418;  
RA Matthysens G., Rabbitts T.H.,  
RT "Structure and multiplicity of genes for the human immunoglobulin  
RT heavy chain variable region."  
RJ Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J00236; AAA53516.1; -.  
CC EMBL: M35415; AAA58735.1; -.  
CC PIR: A02047; H3HU26.  
CC InterPro: IPR003006; -.  
CC Pfam: PF00047; Ig; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 72.4%; Score 446; DB 1; Length 117;  
Best Local Similarity 85.7%; Pred. No. 3.5e-38;  
Matches 84; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVOLVESGGVQPGSRSLRLSCAASGFTFSYDMWVRQAPGKLEWAKVSSGGSTYY 60  
DB 20 EVQLLESGGGLVQPGSRSLRLSCAASGFTFSYDMWVRQAPGKLEWAKVSSGGSTYY 79  
QY 61 LDTVOGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98  
DB 80 GDSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAR 117

```

CC      MACROGLOBULIN.
DR      PIR; A02064; M3HUGL.
DR      HSSP; P01772; 2IG2.
DR      InterPro; IPR003006; -.
DR      Pfam; PF00047; ig.1.
DR      KW      Immunoglobulin V region.
DR      NON_TER 116
FT      SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match          71.7%; Score 441.5; DB 1; Length 116;
Best Local Similarity 71.8%; Pred. No. 9.7e-38;
Matches 84; Conservative 12; Mismatches 20; Indels 1; Gaps:

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYDMSWVRQAPGKLEWAKVSGGGSTYY 60
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 EVQLVESGGDLVQPGKSLRLSCAASGFBFBGLGTMVTRQAPGKLEWVANIKZBGSZBY 60
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY      61 LPTVQGRTTISRDNSKNTLYLQMNSLRADPTAVYYCARHNHNGSFAYWGQGTFTTVTSS 117
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 VDSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCAR-GWGGGDYWGQGTLLTVTST 116
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT      9
HV3H_HUMAN ID HV3H_HUMAN STANDARD; PRT; 122 AA.
AC      P01769;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG HEAVY CHAIN V-III REGION CA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

[1]  
MEDLINE=74175307; PubMed=4208843;  
Florent G., Lehman D., Putnam F.W.;  
"The switch point in mu heavy chains of human IgM immunoglobulins."  
Biochemistry 13:2482-2498(1974).  
- I - MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
MACROGLOBULIN.  
PIR; A02052; M3HUGA.  
HSPP; P01772; ZIG2.  
InterPro: IPR003066.

KW	immunoglobulin v region.
FT	MOD_RES 1 1
FT	NON_TER 122 122
SQ	SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;
Query Match 71.7%; Score 441.5; DB 1; Length 122; Best Local Similarity 67.2%; Pred. No. le-37; Matches 82; Conservative 19; Mismatches 16; Indels 5; Gaps	
QY	1 QVQLVESGGGVQPGRSRLSCAASGTFSSYDMSWVRQAPGKLEWAKVYSGGGSITY 60
DB	1 QVZLVZSGGGAVZPGRSLRSLCAASGFSFSTYAMHWVRQAPGKGLZWLSIVSYBGHBZY 11
QY	61 LDTVGGRFTISRDNSKNLTLYLQMNSLRADPAVYYCARHN--YGSAF---YWGQGTTVTV 12
DB	61 ASNVKGRFTISRBSKBPTWMELMSLRANTAVYYCARGIALGSVAGTDYWGZGLTVI 12
QY	116 SS 117    121 SS 122
RESULT 10	
HV55_MOUSE	
ID HV55_MOUSE	PRT; 117 AA.

```
AC 18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J03052; HVMS34.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 50 58 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 3.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 69.5%; Score 428; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 2.2e-36;
Matches 80; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVKPGGSLKLSAASGFAFSSYDMSWVRQTPKRLWVAYISSGGSTYY 79
Qy 61 LDTVGQRTISRDNKNTLYLQMSLRAEDTAVYYCAR 98
Db 80 PDKVGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR 117

RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
```

```
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 68.8%; Score 424; DB 1; Length 115;
Best Local Similarity 69.2%; Pred. No. 5.5e-36;
Matches 81; Conservative 20; Mismatches 14; Indels 2; Gaps 2;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVETGGGLIQPGKSLRLSCAASGFTVBSHMSWVRQAPGKALZWSAIYR-GGTYIY 59
Qy 61 LDTVGQRTISRDNKNTLYLQMSLRAEDTAVYYCARHNYGSFAYWGQGTITVVS 117
Db 60 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYYCAR-DLAAARLFKGGTITVVS 115

RESULT 12
HV3L_HUMAN
ID HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; ALHUBR.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 68.7%; Score 423; DB 1; Length 119;
Best Local Similarity 69.5%; Pred. No. 7.2e-36;
Matches 82; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
Db 1 QVQLVESGGGVQAGTSLRLSCTSAFNLSDYAMHWVRQAPGKGLZWALISYGGSTYY 60
Qy 61 LDTVGQRTISRDNKNTLYLQMSLRAEDTAVYYCAR--HNYGSFAYWGQGTITVVS 116
Db 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKLIIVAGTRBFWGQGLTVTS 118

RESULT 13
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
```

```

-0X NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR: B28966;
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 67.9%; Score 418.5; DB 1; Length 116;
Best Local Similarity 83.7%; Pred. No. 2e-35;
Matches 82; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVSGGTVQPGKSLRSLSCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 20 EVQLVSGGGLVQPGGSLKSLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 78
QY 61 LDTVQGRFTISRDNKNTLYLQNSLRADETAVYYCAR 98
DB 79 ADSVGRFTISRDNKNTLYLQNSLRADETAVYYCAR 116

RESULT 14
HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/CJ;
RA Levine N.S., Malipiero U.V., Lebecqz S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH1783 SUBFAMILY.
DR PIR: JTO505; HVMS84.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

```

```

Query Match 67.9%; Score 418; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 2.2e-35;
Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGGTVQPGKSLRSLSCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 20 EVKLVEGGGLVQPGGSLKSLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQNSLRADETAVYYCAR 98
DB 80 PDTVKGRTISRDNKNTLYLQNSLRADETAVYYCAR 117

RESULT 15
HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR: A02077; AVMSX4.
DR HSP: P01810; 2FEJ.
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin v region.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

```

```

Query Match 67.5%; Score 415.5; DB 1; Length 119;
Best Local Similarity 65.3%; Pred. No. 4.1e-35;
Matches 77; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVSGGTVQPGKSLRSLSCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
DB 1 EVKLVEGGGLVQPGGSLKSLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQNSLRADETAVYYCAR-HNYGSFAYWGCGTTVTSS 117
DB 61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDALYYCARLHYGYAAYWGCGTLVTVA 118

```

Search completed: October 11, 2001, 12:08:43  
Job time: 403 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:00:45 ; Search time 46.3 Seconds

(without alignments)  
334.335 Million cell updates/sec

Title: US-08-791-391a-2

Perfect score: 616

Sequence: 1 QVQVLESGGVQPGRLSLR.....RHNYGSFAYWGQTTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	78.4	116	4 Q9UL93	Q9UL93 homo sapien
2	475	77.1	113	4 Q9UL90	Q9UL90 homo sapien
3	474	76.9	121	4 Q9UL71	Q9UL71 homo sapien
4	464.5	75.4	147	4 Q9Y509	Q9Y509 homo sapien
5	460.5	74.8	118	4 Q9UL72	Q9UL72 homo sapien
6	460.5	74.8	122	4 Q9UL84	Q9UL84 homo sapien
7	459.5	74.6	112	4 Q9HCC1	Q9HCC1 homo sapien
8	458.5	74.4	118	4 Q9UL91	Q9UL91 homo sapien
9	419	68.0	131	4 Q9UL88	Q9UL88 homo sapien
10	414	67.2	95	4 Q9UL86	Q9UL86 homo sapien
11	403.5	65.5	298	11 Q9QIF0	Q9QIF0 mus musculus
12	403.5	65.5	437	11 Q9RIA4	Q9RIA4 mus musculus
13	382.5	62.1	124	4 Q9UL92	Q9UL92 homo sapien
14	372	60.4	104	4 Q9UL87	Q9UL87 homo sapien
15	366	59.4	112	4 Q9UGP3	Q9UGP3 homo sapien
16	351.5	57.1	124	6 Q9N0M4	Q9N0M4 oryctolagus
17	349	56.7	125	4 Q9UL95	Q9UL95 homo sapien
18	348.5	56.6	124	6 Q9N0W6	Q9N0W6 oryctolagus
19	339	55.0	117	11 Q9QXE9	Q9QXE9 mus musculus

20	336.5	54.6	118	11 Q9Z1C4	Q9Z1C4 mus musculus
21	336	54.5	119	5 Q9QY22	Q9QY22 schistosoma
22	333	54.1	117	11 Q9QXF0	Q9QXF0 mus musculus
23	331.5	53.8	116	4 Q9UL89	Q9UL89 homo sapien
24	325	52.8	119	4 Q9UL94	Q9UL94 homo sapien
25	317.5	51.5	109	11 Q9JL75	Q9JL75 mus musculus
26	312	50.6	119	4 Q9UL73	Q9UL73 homo sapien
27	307	49.8	157	4 Q9S978	Q9S978 homo sapien
28	306.5	49.8	110	11 Q9JL83	Q9JL83 mus musculus
29	306	49.7	150	4 Q9Y298	Q9Y298 homo sapien
30	304.5	49.4	150	4 Q9S973	Q9S973 homo sapien
31	302	49.0	77	4 Q9S741	Q9S741 homo sapien
32	297	48.2	109	11 Q9JL85	Q9JL85 mus musculus
33	296.5	48.1	110	11 Q9JL77	Q9JL77 mus musculus
34	292.5	47.5	114	11 Q9JL81	Q9JL81 mus musculus
35	292.5	47.5	122	4 Q9UL75	Q9UL75 homo sapien
36	292	47.4	82	4 Q9S729	Q9S729 homo sapien
37	290.5	47.2	77	4 Q9S726	Q9S726 homo sapien
38	290	47.1	117	11 Q9Z1C6	Q9Z1C6 mus musculus
39	288	46.8	78	4 Q9S730	Q9S730 homo sapien
40	286.5	46.5	77	4 Q9S728	Q9S728 homo sapien
41	286	46.4	102	11 Q9JL79	Q9JL79 mus musculus
42	276.5	44.9	416	4 Q9NPP6	Q9NPP6 homo sapien
43	274	44.5	79	4 Q9S731	Q9S731 homo sapien
44	274	44.5	81	4 Q9S719	Q9S719 homo sapien
45	268.5	43.6	86	4 Q9S722	Q9S722 homo sapien

ALIGNMENTS

RESULT 1					
Q9UL93					
ID Q9UL93	PRELIMINARY	PRT	116 AA.		
AC Q9UL93					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)					
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=98277139; PubMed=9614934;					
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,					
RA Young D.C.;					
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal					
RT fetus.";					
RL Clin. Immunol. Immunopathol. 87:184-192(1998).					
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX					
CC DOMAIN.					
DR EMBL; AF035021; AAD56257.1; -.					
DR InterPro; IPR003006; -.					
DR InterPro; IPR003596; -.					
DR Pfam; PF00047; ig; 1.					
DR SMART; SM00406; Igv; 1.					
FT NON_TER 1 116					
FT NON_TER 116 116					
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;					
Query Match	78.4%	Score 483;	DB 4;	Length 116;	
Best Local Similarity	81.0%	Pred. No. 2e-43;	17;	Indels	0;
Matches	94;	Conservative	5;	Mismatches	0;
QY 2 VOLVESGGVQPGRLSLRSLRCAASGFTFSYDMSVWROAPGKGLWVAKVSGGGSTYVL 61					
DB 1 VOLVESGGVQPGRLSLRSLRCAASGFTFSYAHVWROAPGKGLWVAVISDGSNKYYA 60					
QY 62 DTVQGRFTISDRNSKNTLYLQMNLSRAEDTAVYYCARHNYGSFAYWGQTTVTSS 117					

Db 61 DSVKGRFTISRDNKNTLYLQMSLSRAEDTAMYACAGGGGLGLGWGQGLTVTVSS 116

RESULT 2

Q9UL90 ID Q9UL90 PRELIMINARY; PRT; 113 AA.

AC Q9UL90;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL; AF035024; AAD56260.1; -.

DR InterPro; IPR003006; -.

DR InterPro; IPR003596; -.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00406; IGV; 1.

FT NON\_TER 1 113

FT NON\_TER 113 113

SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 77.1%; Score 475; DB 4; Length 113;

Best Local Similarity 79.5%; Pred. No. 1.4e-42;

Matches 93; Conservative 6; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMVSRQAPGKGLWVAVIRYDGSNKYY 60

Db 1 EVQLVESGGGVQPGKSLRSCAASGFTSSYGMHWVRQAPGKGLWVAFIRYDGSNKYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAHNYGSFYWGQGLTVTVSS 117

Db 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAK----DLNFWGQGLTVTVSS 113

RESULT 3

Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.

AC Q9UL71;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL; AF035043; AAD56279.1; -.

DR HSSP; P01772; 2FBA.

DR InterPro; IPR003006; -.

DR InterPro; IPR003596; -.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON\_TER 1 121

FT NON\_TER 121 121

SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 76.9%; Score 474; DB 4; Length 121;

Best Local Similarity 76.0%; Pred. No. 1.9e-42;

Matches 92; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMVSRQAPGKGLWVAVIRYDGSNKYY 60

Db 1 EVQLVESGGGVQPGKSLRSCAASGFTFDGYAMHWVRQAPGKGLWVSLISDGGSTYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAHNYGSFYWGQGLTVTVSS 116

Db 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTALYYCAKGVKVTIYDRFDIWGQGLTVTVSS 120

QY 117 S 117

Db 121 S 121

RESULT 4

Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.

AC Q9Y509;

DT 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

DE VH3 PROTEIN (FRAGMENT).

GN VH3

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96071149; PubMed=7475288;

RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,

RA Lichtenstein A.K., Berenson J.R.;

RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers.";

RL Leukemia 9:1948-1953(1995).

CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL; S80860; AAD14339.1; -.

DR HSSP; P01772; 2FBA.

DR InterPro; IPR003006; -.

DR InterPro; IPR003596; -.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON\_TER 1 147

FT NON\_TER 147 147

SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 75.4%; Score 464.5; DB 4; Length 147;

Best Local Similarity 71.4%; Pred. No. 2.4e-41;

Matches 90; Conservative 9; Mismatches 18; Indels 9; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRSCAASGFTSSYDMVSRQAPGKGLWVAVIRYDGSNKYY 60

Db 1 QVHLVESGGGVQPGKSLRSCAASGFTFTYGMVSRQAPGKGLDWALISYDGSQYY 60

QY 61 LDTVQGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAR-----HNYSFYWGQGLT 111

Db 61 AGSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAKDGNYFSDYSVGYIAGIDYWGQGT 120

QY 112 TVTVSS 117

Db 121 LTVTVSS 126



```
RESULT 5
Q9UL72
ID Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DE 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 118;
Best Local Similarity 78.2%; Pred. No. 4.8e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 3; Gaps 2;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGLVQPGKSLRLCAASGFTVSSNMVWRQAPGKLGESVS-VYISGGSYY 59

Qy 61 LDTVGRTISRDNKNTLYLQMSLRADTAIVYICARHNYGSFA--YWGQGTITVSS 117
Db 60 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARDFGEFLDYWGQGTITVSS 118

RESULT 6
Q9UL84
ID Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DE 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; -.

```

```
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 122;
Best Local Similarity 73.8%; Pred. No. 5e-41;
Matches 90; Conservative 10; Mismatches 17; Indels 5; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60

Qy 61 LDTVGRTISRDNKNTLYLQMSLRADTAIVYICARHNYGS----FAYWGQGTITV 115
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARHNYGS----FAYWGQGTITV 120

Qy 116 SS 117
Db 121 SS 122

RESULT 7
Q9HCC1
ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : isolation from a
RT synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
FT NON_TER 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 74.6%; Score 459.5; DB 4; Length 112;
Best Local Similarity 77.0%; Pred. No. 5.7e-41;
Matches 87; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGKSLRLCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVESGGGVVQPGKSLRLCAASGFTFDDYGMVWRQAPGKLEWVSGINWNGSGTGY 60

Qy 61 LDTVGRTISRDNKNTLYLQMSLRADTAIVYICARHNYGSFAYWGQGTIV 113
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYICARRRY-ALDYWGQGTIV 112

RESULT 8
Q9UL91
ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035023; AAD56259.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 74.4%; Score 458.5; DB 4; Length 118;
Best Local Similarity 76.9%; Pred. No. 7.7e-41;
Matches 90; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVQVSGGGVQVQGRSLRLSCLASGFTFSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQVSGGGVQVQGRSLRLSCLASGFTFSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LDTVQGRFTISRDNKNTLYQMNSLRADTAVYYCARHNYG-SFAYWGQGTWTVVS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRADTAVYYCARGDSSEAFDVGQGTWTVVS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ID Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035026; AAD56262.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 68.0%; Score 419; DB 4; Length 131;
Best Local Similarity 65.6%; Pred. No. 1.2e-36;
Matches 86; Conservative 10; Mismatches 21; Indels 14; Gaps 2;

QY 1 QVQVSGGGVQVQGRSLRLSCLASGFTFSYDMSWVRQAPGKLEWVAKVSS--GGGST 58
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQVSGGGVQVQGRSLRLSCLASGFTFSKAWMSWVRQAPGKLEWVGRKSKTDGGTT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 59 YYLDTVQGRFTISRDNKNTLYQMNSLRADTAVYYC-----ARHNYGSFAY 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DYAAPVKGRLTISRDSSKNTLYLRMSLKTADTAVYYCTGITMIIVITSSKRTSFY 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 107 WGQGTWTVSS 117
:|||||:|||||
Db 121 WGQGTWTVSS 131
:|||||:|||||

RESULT 10
ID Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 67.2%; Score 414; DB 4; Length 95;
Best Local Similarity 82.1%; Pred. No. 2.8e-36;
Matches 78; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 VQVQVSGGGVQVQGRSLRLSCLASGFTFSYDMSWVRQAPGKLEWVAKVSSGGSTYYL 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VQLESGGGVQVQGRSLRLSCLASGFTFSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 DTVQGRFTISRDNKNTLYQMNSLRADTAVYYC 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DSVKGRFTISRDNKNTLYQMNSLRADTAVYYC 95
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
```



```

DR InterPro: IPR003600; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E9E7B CRC64;

Query Match 60.4%; Score 372; DB 4; Length 104;
Best Local Similarity 70.2%; Pred. No. 8.1e-32;
Matches 73; Conservative 9; Mismatches 14; Indels 8; Gaps 2;

QY 22 CAASGTFSSYDMRWQAPGKGLWVAKVSGGGSTYYLDTVQGRFTISRDNKNTLYL 81
   |||||  |  |||||  |||||  :  ||  |  |||||  |||||  |||||
Db 1 CAASGTFDDYAMHWVQAPGKGLWVSGISWNSGSGIGYADSVKGRFTISRDNKNSLYL 60
   |||||  |||||  |||||  |||||  ||  |  |||||  |||||  |||||
QY 82 QMNSLRAEDTAVTYCARHNY---GS-----FAYWGQGTVTYVSS 117
   |||||  |||||  |||||  ||  ||  |  |||||  |||||
Db 61 QMNSLRAEDTALYCAKANYGSGSYTYEFQHWGQGTLYTVSS 104

RESULT 15
Q9UGP3 PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IMMUNOBULBULIN HEAVY CHAIN (FRAGMENT).
GN IGH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Zafiroopoulos A., Kandilgiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RT "Induction of somatic mutations in human B cells by in vitro
RT immunization.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ132560; CAB65078.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;

Query Match 59.4%; Score 366; DB 4; Length 112;
Best Local Similarity 67.6%; Pred. No. 3.8e-31;
Matches 71; Conservative 10; Mismatches 12; Indels 12; Gaps 1;

QY 18 LRLSCAASGTFSSYDMRWQAPGKGLWVAKVSGGGSTYYLDTVQGRFTISRDNKSN 77
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 LRLSCAASGTFSSYDMRWQAPGKGLWVAKVSGGGSTYYLDTVQGRFTISRDNKSN 77
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 78 TLYLQNSLRAEDTAVTYCARHNYGSFA-----YWGQG 110
   |||||  |||||  |||||  |||||  |||||  |||||
Db 61 TLYLQNSLRAEDTAVTYCARHNYGSFA-----YWGQG 105
   |||||  |||||  |||||  |||||  |||||  |||||

```

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 11:45:50 ; Search time 44.8 Seconds

(without alignments)  
158.326 Million cell updates/sec

Title: US-08-791-391a-2

Perfect score: 616

Sequence: 1 QVQLVESGGGVVQPGRLRL.....RHNYGSFAYWGQTTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_0601.\*
- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*
  - 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*
  - 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*
  - 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*
  - 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*
  - 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*
  - 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.\*
  - 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*
  - 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*
  - 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*
  - 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*
  - 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*
  - 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*
  - 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*
  - 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.\*
  - 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*
  - 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.\*
  - 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.\*
  - 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*
  - 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*
  - 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*
  - 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	117	AAW76001	Vitaxin antibody h
2	616	100.0	117	AAW76001	Vitaxin heavy chain
3	552	89.6	117	AAW76003	LM609 antibody hea
4	552	89.6	117	AAW76003	Antibody LM609 hea
5	539	87.5	117	AAW7526	Heavy chain variab
6	539	87.5	239	AAW73874	Human antiFc epsil
7	539	87.5	242	AAW73876	Human antiFc epsil
8	536	87.0	117	AAW06381	Murine monoclonal
9	525	85.2	130	AAW06379	Murine monoclonal
10	523.5	85.0	118	AAW7591	Chimeric antibody
11	523.5	85.0	118	AAW89636	Human antibody hea

12	523.5	85.0	118	21	AAW77512	Peptide seq ID No:
13	523.5	85.0	118	22	AAW76890	Human antibody H c
14	523.5	85.0	118	22	AAW76909	Human antibody H c
15	523.5	85.0	118	22	AAW76928	Human antibody H c
16	523.5	85.0	137	19	AAW57603	Chimeric antibody
17	523.5	85.0	137	20	AAW89635	Human antibody hea
18	523.5	85.0	137	21	AAW77514	Peptide encoded by
19	517.5	84.0	139	15	AAW52823	Humanised murine K
20	517.5	84.0	139	16	AAW70471	Humanised anti-KC-
21	517.5	84.0	240	20	AAW02472	A single chain ant
22	517	83.9	121	20	AAW86122	Protein sequence o
23	514	83.4	245	22	AAW67620	Human leukocyte an
24	509.5	82.7	139	18	AAW21652	Humanised reshaped
25	509	82.6	119	22	AAW62088	Human Vh consensus
26	509	82.6	119	22	AAW60401	Consensus human he
27	509	82.6	119	22	AAW61586	Human variable hea
28	509	82.6	240	21	AAW15124	Anti-human CTLA-4
29	509	82.6	240	21	AAW15125	Anti-murine CTLA-4
30	508	82.5	121	20	AAW86120	Protein sequence o
31	508	82.5	138	21	AAW32406	Mouse anti-verotox
32	505	82.0	113	19	AAW70621	Human consensus fr
33	505	82.0	113	21	AAW82347	Human consensus se
34	503.5	81.7	443	18	AAW13564	Humanised anti-L-S
35	503	81.7	117	20	AAW86137	Protein sequence o
36	502	81.5	119	14	AAW32240	Humanised MAB hea
37	501.5	81.4	120	18	AAW27553	Human Ab heavy cha
38	501.5	81.4	281	18	AAW27560	Consensus single c
39	500.5	81.2	118	22	AAW67508	Light chain variab
40	500.5	81.2	118	22	AAW67513	Heavy chain variab
41	500.5	81.2	131	18	AAW13520	Anti-melanoma antl
42	500.5	81.2	143	21	AAW82629	Human PTHrP monocl
43	500	81.2	117	19	AAW48866	Chimeric humanized
44	500	81.2	117	20	AAW86135	Protein sequence o
45	500	81.2	264	19	AAW73049	Humanised A33 SCAB

## ALIGNMENTS

RESULT 1

AAW76001  
ID AAW76001 standard; Protein; 117 AA.

XX AC AAW76001;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAW49820.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Claim 1; Fig 1a; 129pp; English.  
 XX This sequence represents a fragment of the vitaxin antibody variable  
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to  
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3  
 CC to a ligand and thus block integrin-mediated signal transduction. This is  
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated  
 CC disease, specifically angiogenesis and restenosis (but also e.g.  
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,  
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,  
 CC osteoporosis etc.). The antibodies contain non-murine framework regions  
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity  
 CC more than 90 times greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 616; DB 19; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-49;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWAKVSSGGSTYY 60  
 |||||  
 Db 1 qvqlvesgggvqpgrslrlscaasgftfssydmwvrrqapkgglewkvssggstyy 60  
 |||||

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTVVYCARHNYGSFAYWGCGTTVTSS 117  
 |||||  
 Db 61 ldtvqgrftisrdnskntlylqmslraedtavvycarhnygsfaywgggtvtvss 117  
 |||||

## RESULT 2

AA61359  
 ID AAB61359 standard; protein; 117 AA.

XX  
 AC AAB61359;

XX  
 DT 03-APR-2001 (first entry)

XX Vitaxin heavy chain variable region protein.

XX  
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX  
 OS Unidentified.

XX  
 PN WO200078815-A1.

XX  
 PD 28-DEC-2000.

XX  
 PF 23-JUN-2000; 2000WO-US17454.

XX  
 PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX  
 PI Huse WD, Wu H;

XX  
 XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 616; DB 22; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-49;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLEWAKVSSGGSTYY 60  
 |||||  
 Db 1 qvqlvesgggvqpgrslrlscaasgftfssydmwvrrqapkgglewkvssggstyy 60  
 |||||

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTVVYCARHNYGSFAYWGCGTTVTSS 117  
 |||||  
 Db 61 ldtvqgrftisrdnskntlylqmslraedtavvycarhnygsfaywgggtvtvss 117  
 |||||

## RESULT 3

AAW76003  
 ID AAW76003 standard; Protein; 117 AA.

XX  
 AC AAW76003;

XX  
 DT 02-NOV-1998 (first entry)

XX LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis.

XX  
 OS Mus sp.

XX  
 PN WO9833919-A2.

XX  
 PD 06-AUG-1998.

XX  
 PF 30-JAN-1998; 98WO-US01826.

XX  
 PR 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX  
 PI Glaser SM, Huse WD;

XX  
 XX WPI; 1998-437472/37.

XX  
 XX N-PSDB; AAV49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

XX This sequence represents the LM609 antibody variable heavy chain region.  
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 89.6%; Score 552; DB 19; Length 117;  
 Best Local Similarity 88.0%; Pred. No. 1.7e-43;  
 Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPCGSRSLRLSCAASGFTFSYDMSWVRQAPCKGLEWVAKVSSGGSTYY 60  
 Db 1 evqlvesgggvlvpgfslrlscaasgftfssydmwvrqapckglewvkvssgggstyy 60  
 Qy 61 LDTVOGRETISRDNKNTLYLQMSLRAEDTAVYYCARHNYGSPFAYWGQGTVTYVSS 117  
 Db 61 ldtvggrftisrdnakntlylqmslnsedtamyycarhnygsfaywgqgtltvtvsa 117

RESULT 4

AAB61361  
 ID AAB61361 standard; protein; 117 AA.

XX AAB61361;

DT 03-APR-2001 (first entry)

DE Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO20007815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

PS Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX Sequence 117 AA;

Query Match 89.6%; Score 552; DB 22; Length 117;  
 Best Local Similarity 88.0%; Pred. No. 1.7e-43;

Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPCGSRSLRLSCAASGFTFSYDMSWVRQAPCKGLEWVAKVSSGGSTYY 60  
 Db 1 evqlvesgggvlvpgfslrlscaasgftfssydmwvrqapckglewvkvssgggstyy 60

Qy 61 LDTVOGRETISRDNKNTLYLQMSLRAEDTAVYYCARHNYGSPFAYWGQGTVTYVSS 117

Db 61 ldtvggrftisrdnakntlylqmslnsedtamyycarhnygsfaywgqgtltvtvsa 117

RESULT 5

AAW27526  
 ID AAW27526 standard; Protein; 117 AA.

XX AAW27526;

DT 16-DEC-1997 (first entry)

DE Heavy chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;  
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;  
 KW IGE; MAB; heavy chain; variable region; humanised; semi-chimeric;  
 KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX Homo sapiens.

XX JP09191886-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

XX (ASAK ) ASahi BREWERIES LTD.

XX (NIKK-) NIKKA WHISKEY KK.

XX (TORI ) TORII YAKUHEIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

XX high-affinity IgE receptor - useful medicinally and have low

XX antigenicity in humans

XX Claim 2; Page 13; 26pp; Japanese.

XX The present sequence, the heavy chain variable region of the human  
 CC antibody (Ab) CRA2, was used in the preparation of a humanised or  
 CC semi-chimeric monoclonal Ab (MAB), comprising complementary  
 CC determining regions (CDR) from a murine, anti-human high affinity  
 CC immunoglobulin E (IgE) receptor, MAB. The humanised, semi-chimeric  
 CC or chimeric MAB can be used to treat or prevent diseases,  
 CC specifically allergies, associated with the receptor, and has very  
 CC low antigenicity in humans.

XX Sequence 117 AA;

Query Match 87.5%; Score 539; DB 18; Length 117;

Best Local Similarity 86.3%; Pred. No. 2.7e-42;

Matches 101; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPCGSRSLRLSCAASGFTFSYDMSWVRQAPCKGLEWVAKVSSGGSTYY 60  
 Db 1 evqlvesgggvlvpgfslrlscaasgftfssydmwvrqapckglewvafisnrggstyy 60

Qy 61 LDTVOGRETISRDNKNTLYLQMSLRAEDTAVYYCARHNYGSPFAYWGQGTVTYVSS 117

Db 61 potvkggrftisrdnakntlylqmslnsedtavyycarhnygmdywgqgttvtvss 117







XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX PI Sato K, Wakahara Y, Yabuta N;  
 XX PS WPI; 1998-230640/20.  
 XX DR  
 XX CC New chimeric antibodies against human parathormone related  
 PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other  
 PT disorders caused by malignant neoplasm(s)  
 XX CC  
 XX PS Claim 21; Page 120; 182pp; Japanese.  
 XX CC  
 XX CC New antibodies have been developed which are specific for human  
 CC parathormone related peptides (hPTHrP). The antibodies comprise chimeric  
 CC L and/or H chains, where the C region is of human and L region of mouse,  
 CC origin. The present sequence represents a specifically claimed region of  
 CC an antibody of the invention. Host cells, transformed with vectors  
 CC containing DNA encoding antibodies of the invention, can be used to  
 CC produce the antibodies. The antibodies may be used to treat  
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of  
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,  
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They  
 CC may also be used for treatment of hypophosphoemia such as that due to  
 CC pathogens or to vitamin D resistance.  
 XX CC  
 XX SQ Sequence 118 AA;

Query Match 85.0%; Score 523.5; DB 19; Length 118;  
 Best Local Similarity 87.3%; Pred. No. 7.1e-41;  
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGRLSLRSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60  
 Db 1 qvqlvesgggvqpgrrlsrscasgftfssygmwvrqpgkglewatissggsytyy 60  
 QY 61 LDTVQGRFTISRDNKNTLYQMNSLRRAEDTAVYICARHNYGS-FAYWGOGTTVTVSS 117  
 Db 61 pdsvkgrftisrdnsnkntlyqmnsrleadtavycarqtmtyfaywgggtlvtvss 118

RESULT 11  
 AAW89636  
 ID AAW89636 standard; Protein; 118 AA.  
 XX AC AAW89636;  
 XX DT 14-APR-1999 (first entry)  
 XX DE Human antibody heavy chain mature protein.  
 XX KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;  
 KW Inhibitor; humanised.  
 XX OS Homo sapiens.  
 XX PN WO9851329-A1.  
 XX PD 19-NOV-1998.  
 XX PF 13-MAY-1998; 98WO-JP02116.  
 XX PR 18-JUL-1997; 97JP-0194445.  
 XX PR 15-MAY-1997; 97JP-0125505.  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX PI Ishii K, Sato K, Tunenari T;  
 XX WPI; 1999-070101/06.  
 XX PT Inhibitors of binding of parathyroid hormone related peptide to its

PT receptor - useful for, e.g. treatment of cachexia arising from  
 PT cancer or other diseases  
 XX CC  
 XX PS Example 4; Page 81; 125pp; Japanese.  
 XX CC  
 XX CC The present invention describes compositions for the treatment of  
 CC cachexia containing a substance which inhibits the binding of a  
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an  
 CC active component. This substance may be an antagonist to the receptor,  
 CC or an antibody (preferably monoclonal) or an antibody fragment,  
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.  
 CC The present invention also describes a humanised antibody prepared  
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for  
 CC the treatment of cachexia arising in connection with diseases such as  
 CC cancer, thereby improving the quality of life of the patient. The  
 CC present sequence represents a human antibody heavy chain from the  
 CC present invention.  
 XX CC  
 XX SQ Sequence 118 AA;

Query Match 85.0%; Score 523.5; DB 20; Length 118;  
 Best Local Similarity 87.3%; Pred. No. 7.1e-41;  
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGRLSLRSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60  
 Db 1 qvqlvesgggvqpgrrlsrscasgftfssygmwvrqpgkglewatissggsytyy 60  
 QY 61 LDTVQGRFTISRDNKNTLYQMNSLRRAEDTAVYICARHNYGS-FAYWGOGTTVTVSS 117  
 Db 61 pdsvkgrftisrdnsnkntlyqmnsrleadtavycarqtmtyfaywgggtlvtvss 118

RESULT 12  
 AAY77512  
 ID AAY77512 standard; Protein; 118 AA.  
 XX AC AAY77512;  
 XX DT 26-APR-2000 (first entry)  
 XX DE Peptide seq ID No: 56.  
 XX KW Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.  
 XX OS Homo sapiens.  
 XX PN WO200000219-A1.  
 XX PD 06-JAN-2000.  
 XX PF 25-JUN-1999; 99WO-JP03433.  
 XX PR 26-JUN-1998; 98JP-0180143.  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX PI Sato K, Tsunenari T;  
 XX WPI; 2000-117115/10.  
 XX PT Treatment of hypercalcaemic crisis with a substance inhibiting binding  
 PT of parathyroid hormone related peptide to its receptor -  
 XX Example.4; Page 95-96; 120pp; Japanese.  
 XX CC The invention relates to a method of treatment of hypercalcaemic crisis.  
 CC A composition for the treatment of hypercalcaemic crisis contains as  
 CC active component a substance which inhibits the binding of parathyroid  
 CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used  
 CC for the treatment of hypercalcaemic crisis, such as that associated with  
 CC a malignant tumour.







THIS PAGE BLANK (USPTO)

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 11:45:50 ; Search time 25.17 Seconds  
(without alignments)  
95.712 Million cell updates/sec

Title: US-08-791-391a-2

Perfect score: 616

Sequence: 1 QVQLVESGGGVQPGRLSLR.....RHNYGSFYWGQGTITVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PT05\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	517.5	84.0	139	1	US-08-129-930B-96
2	505	82.0	113	3	US-08-974-899-6
3	503.5	81.7	135	4	US-08-579-378A-20
4	503.5	81.7	443	5	PCT-US96-13152-4
5	502.5	81.6	122	2	US-07-934-373C-21
6	502.5	81.6	122	3	US-08-437-642B-21
7	502.5	81.6	122	5	PCT-US93-07832-21
8	502	81.5	119	1	US-08-053-171-12
9	502	81.5	125	1	US-08-478-039-99
10	502	81.5	125	1	US-08-476-349A-99
11	500.5	81.2	131	4	US-08-983-607-28
12	500	81.2	117	4	US-08-752-693A-4
13	497.5	80.8	122	5	PCT-US93-08435-12
14	497.5	80.8	122	5	PCT-US93-08435-43
15	496	80.5	119	1	US-07-988-925-11
16	496	80.5	119	2	US-08-362-780-11
17	495	80.4	119	1	US-08-331-398A-46
18	495	80.4	119	2	US-08-331-379B-46
19	495	80.4	119	2	US-08-759-804A-46
20	495	80.4	119	5	PCT-US94-07659-6
21	494.5	80.3	117	1	US-07-942-245-36
22	494.5	80.3	122	5	PCT-US93-08435-14
23	494	80.2	120	1	US-07-942-245-35
24	494	80.2	125	2	US-08-428-197-1
25	494	80.2	125	5	PCT-US93-10555-1
26	492.5	80.0	116	4	US-08-983-607-36
27	491	79.7	123	2	US-08-665-202-30

28	489.5	79.5	120	2	US-07-934-373C-4	Sequence 4, Appli
29	489.5	79.5	120	3	US-08-437-642B-4	Sequence 4, Appli
30	489	79.4	119	1	US-08-207-996-22	Sequence 22, Appl
31	489	79.4	119	2	US-08-760-840A-22	Sequence 22, Appl
32	489	79.4	119	3	US-09-266-119-22	Sequence 22, Appl
33	489	79.4	120	2	US-08-428-197-20	Sequence 20, Appl
34	489	79.4	120	5	PCT-US93-10555-20	Sequence 20, Appl
35	488.5	79.3	135	4	US-08-619-491-8	Sequence 8, Appli
36	487	79.1	117	2	US-08-652-558-44	Sequence 44, Appl
37	487	79.1	120	2	US-08-428-197-22	Sequence 22, Appl
38	487	79.1	120	5	PCT-US93-10555-22	Sequence 22, Appl
39	486	78.9	117	2	US-08-652-558-46	Sequence 46, Appl
40	486	78.9	117	4	US-08-983-607-46	Sequence 46, Appl
41	486	78.9	120	2	US-08-428-197-24	Sequence 24, Appl
42	486	78.9	120	2	US-08-428-197-26	Sequence 26, Appl
43	486	78.9	120	2	US-08-428-197-28	Sequence 28, Appl
44	486	78.9	120	5	PCT-US93-10555-24	Sequence 24, Appl
45	486	78.9	120	5	PCT-US93-10555-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-08-129-930B-96  
; Sequence 96, Application US/08129930B  
; Patent No. 5804187  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Broad  
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
; TITLE OF INVENTION: Diagnostic Vaccination and  
; TITLE OF INVENTION: Therapeutic Methods  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: V. AMZEL & ASSOC.  
; STREET: 2055 No. 5804187th Broadway, Suite 201  
; CITY: Walnut Creek  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94596

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,930B  
FILING DATE: September 30, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel Ph.D., Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: CRECC-008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 521-1333  
TELEFAX: (510) 521-3541  
TELEX: n.a.  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-129-930B-96

Query Match 84.0%; Score 517.5; DB 1; Length 139;  
Best Local Similarity 83.3%; Pred. No. 7.4e-46;  
Matches 100; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

```

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNSWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQVSEGGGLVPGGSLRLSCAASGFAFSSYAMSWVRQAPGKLEWVAEISSGGNYAY 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARHNYGS---PAYWGQGTFTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 QDVTGRTISRDNKNTLYLQMSLRRAEDTAVYYCAREDTGIPAFYWGQGTFTVSS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P101R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-6

Query Match 82.0%; Score 505; DB 3; Length 113;
Best Local Similarity 83.8%; Pred. No. 1.1e-44;
Matches 98; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNSWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLSEGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSVISGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARHNYGSFAYWGQGTFTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRTISRDNKNTLYLQMSLRRAEDTAVYYCAR----GFYWGQGTFTVSS 113
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with

```

```

; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

Query Match 81.7%; Score 503.5; DB 4; Length 135;
Best Local Similarity 83.8%; Pred. No. 1.9e-44;
Matches 98; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMNSWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLSEGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVASIST-GGSTYY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRRAEDTAVYYCARHNYGSFAYWGQGTFTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 PDSVKGRTISRDNKNTLYLQMSLRRAEDTAVYYCARDYDGYFDYWGQGTFTVSS 135
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```





FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-21

Query Match 81.6%; Score 502.5; DB 3; Length 122;  
Best Local Similarity 80.3%; Pred. No. 2.2e-44;  
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLWVAKVSSGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSVISGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 LDTVQGRFTISRDNKNTLYQMNSLRRAEDTAVYYCARHNY-----GSFAYWGQGTITV 115  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRRAEDTAVYYCARGRVGYSLSGLYDYGQGTITV 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 116 SS 117  
:||  
Db 121 SS 122

RESULT 7  
PCT-US93-07832-21  
Sequence 21, Application PC/TUS9307832  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07832  
FILING DATE: 19930820  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 13-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 709P2PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US93-07832-21  
Query Match 81.6%; Score 502.5; DB 5; Length 122;  
Best Local Similarity 80.3%; Pred. No. 2.2e-44;  
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSVWRQAPGKGLWVAKVSSGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSVISGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 LDTVQGRFTISRDNKNTLYQMNSLRRAEDTAVYYCARHNY-----GSFAYWGQGTITV 115  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRRAEDTAVYYCARGRVGYSLSGLYDYGQGTITV 120  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 116 SS 117  
:||  
Db 121 SS 122  
RESULT 8  
US-08-053-171-12  
Sequence 12, Application US/08053171  
Patent No. 5562903  
GENERAL INFORMATION:  
APPLICANT: CO, Loibner  
TITLE OF INVENTION: Antibody Derivatives  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,171  
FILING DATE: 22-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-54-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..119  
OTHER INFORMATION: /note= "Sequence of Humanized  
Patent No. 5562903  
OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant  
OTHER INFORMATION: H-hu-BR55-2/1"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 31..35

OTHER INFORMATION: /note= "Complementarity-determining  
OTHER INFORMATION: region"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 50..66  
OTHER INFORMATION: /note= "Complementarity-determining  
OTHER INFORMATION: region"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 99..108  
OTHER INFORMATION: /note= "Complementarity-determining  
OTHER INFORMATION: region"  
US-08-053-171-12

Query Match 81.5%; Score 502; DB 1; Length 119;  
Best Local Similarity 81.5%; Pred. No. 2.4e-44;  
Matches 97; Conservative 13; Mismatches 7; Indels 2; Gaps 2;  
Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKLEWAKVSSGGSTYY 60  
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKLEWAKVSSGGSTYY 60  
Qy 61 LDTVGQRTISRDNSKNTLYLQMSLRAEDTAVYYCAR-HNYGS-FAYWGQGTTLTVSS 117  
Db 61 VDSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARHNYGSFAYWGQGTTLTVSS 119

RESULT 9  
US-08-478-039-99  
Sequence 99, Application US/08478039  
Patent No. 5681722  
GENERAL INFORMATION:  
APPLICANT: Newman, Roland A.  
APPLICANT: Hanna, Nabil  
APPLICANT: Raab, Ronald W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,039  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 18/2  
US-08-478-039-99  
Query Match 81.5%; Score 502; DB 1; Length 125;  
Best Local Similarity 79.2%; Pred. No. 2.5e-44;  
Matches 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;  
Qy 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKLEWAKVSSGGSTYY 60  
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKLEWAKVSSGGSTYY 60  
Qy 61 LDTVGQRTISRDNSKNTLYLQMSLRAEDTAVYYCARHNYGSFAYWGQGTTLTVSS 112  
Db 61 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARHNYGSFAYWGQGTTLTVSS 120  
Qy 113 VTSS 117  
Db 121 VTSS 125  
RESULT 10  
US-08-476-349A-99  
Sequence 99, Application US/08476349A  
Patent No. 5750105  
GENERAL INFORMATION:  
APPLICANT: Newman, Roland A.  
APPLICANT: Hanna, Nabil  
APPLICANT: Raab, Ronald W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-161  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620

```

; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 18/2
;
US-08-476-349A-99

Query Match      81.5%; Score 502; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 2.5e-44;
Matches: 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTFSYDMSVVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVSGGVLVQPGSLRLSCAASGFTFSYAMSVVRQAPGKLEWVAISGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARHNT---YGSFAY----WGQGT 112
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKGVLYYSGSVHWFDPMWCGGTL 120
QY 113 VTVSS 117
Db 121 VTVSS 125

RESULT 11
US-08-983-607-28
; Sequence 28, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 residues
; TYPE: amino acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V13
; FEATURE:
; NAME/KEY: heavy chain
;
US-08-983-607-28

Query Match      81.2%; Score 500.5; DB 4; Length 131;
Best Local Similarity 82.1%; Pred. No. 3.7e-44;
Matches 96; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVQLVSGGVPQGRSLRLSCAASGFTFSYDMSVVRQAPGKLEWAKVSSGGSTYY 60
Db 1 EVQLVSGGVLVQPGSLRLSCAASGFTFSYAMSVVRQAPGKLEWVAISGGSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARHNYGSFYWGQGTFTTVSS 117
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK-GVAPFDYWGQGTPTVSS 116

RESULT 12
US-08-752-693A-4
; Sequence 4, Application US/08752693A
; Patent No. 6190640
; GENERAL INFORMATION:
; APPLICANT: Sydney Welt
; APPLICANT: Gerd Ritter
; APPLICANT: Leonard Cohen
; APPLICANT: Clarence William Jr.
; APPLICANT: Elizabeth Carswell Richards
; APPLICANT: Mary John
; TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA
; USING HUMANIZED ANTIBODIES WHICH
; BIND TO ANTIGEN A33
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PAULINE STASIAK, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,693A
; FILING DATE: 19-No. 6190640-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07321
; FILING DATE: May 21, 1996
; APPLICATION NUMBER: 08/020,223
; FILING DATE: February 16, 1993
; APPLICATION NUMBER: 07/673,153
; FILING DATE: March 18, 1991
; APPLICATION NUMBER: 07/327,765
; FILING DATE: March 23, 1989
; APPLICATION NUMBER: 07/118,411
; FILING DATE: No. 6190640amber 6, 1987
; APPLICATION NUMBER: 06/724,991
; FILING DATE: April 19, 1985

```

Query Match 80.8%; Score 497.5; DB 5; Length 122;

```
Qy      61 LDTVGRFTISRDNSKNTLYLQMNSLRADTAVTYCA--RHNYGSPAYRGQGTTVTSS 117
       |:|:|||||||S|D|N|S|K|N|T|Y|L|Q|M|N|S|L|R|A|D|T|A|V|T|Y|C|A|-|-|H|N|Y|G|S|P|A|Y|R|G|Q|G|T|T|V|T|S|S|
Db      61 RDSVKGRFTISRDNSKNTLYLQMNSLRADTAVTYCAKFQYSGGFEDYWGQGLTVTSS 119
```

Search completed: October 11, 2001, 12:01:06  
Job time: 916 sec

Search completed: October 11, 2001, 12:01:06  
Job time: 916 sec

```
Query Match      80.5%; Score 496; DB 1; Length 119;
Best Local Similarity 79.8%; Pred. No. 9.6e-4;
Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVYPGRSLRLSCAASGFTFSYSDMSWVRQAPKGLWEVAKVSSGGGSTYY 60
    1 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 1 EVQLLESGGVLVPGGSLRLSCAASGFTFSFPMNVRQAPKGLWEVATITLSTGGRTYY 60
```



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:29 ; Search time 2122.65 Seconds  
(without alignments)  
2339.127 Million cell updates/sec

Title: US-08-791-391a-3  
Perfect score: 321  
Sequence: 1 GAGATTGTGCTAACTCAGTC.....GGACCAAGGTGGAATTAAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba1:\*
- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_om:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_pl1:\*
- 13: gb\_pl2:\*
- 14: gb\_pl3:\*
- 15: gb\_pl4:\*
- 16: gb\_bal:\*
- 17: em\_ba2:\*
- 18: em\_fun:\*
- 19: em\_htgo\_hum:\*
- 20: em\_htgo\_inv:\*
- 21: em\_htgo\_rod:\*
- 22: em\_htg\_hum1:\*
- 23: em\_htg\_hum2:\*
- 24: em\_htg\_hum3:\*
- 25: em\_htg\_hum4:\*
- 26: em\_htg\_hum5:\*
- 27: em\_htg\_hum6:\*
- 28: em\_htg\_hum7:\*
- 29: em\_htg\_hum8:\*
- 30: em\_htg\_inv1:\*
- 31: em\_htg\_inv2:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_rod:\*
- 34: em\_hum1:\*
- 35: em\_hum2:\*
- 36: em\_hum3:\*
- 37: em\_hum4:\*
- 38: em\_hum5:\*
- 39: em\_hum6:\*
- 40: em\_hum7:\*
- 41: em\_in:\*
- 42: em\_om:\*
- 43: em\_or:\*

- 44: em\_ov:\*
- 45: em\_pat:\*
- 46: em\_ph:\*
- 47: em\_pl:\*
- 48: em\_ro:\*
- 49: em\_sts:\*
- 50: em\_sy:\*
- 51: em\_un:\*
- 52: em\_vi:\*
- 53: gb\_sts1:\*
- 54: gb\_sts2:\*
- 55: gb\_sts3:\*
- 56: gb\_sy:\*
- 57: gb\_un:\*
- 58: gb\_vil:\*
- 59: gb\_vil2:\*
- 60: gb\_htg1:\*
- 61: gb\_htg2:\*
- 62: gb\_htg3:\*
- 63: gb\_htg4:\*
- 64: gb\_htg5:\*
- 65: gb\_htg6:\*
- 66: gb\_htg7:\*
- 67: gb\_htg8:\*
- 68: gb\_htg9:\*
- 69: gb\_htg10:\*
- 70: gb\_htg11:\*
- 71: gb\_htg12:\*
- 72: gb\_htg13:\*
- 73: gb\_htg14:\*
- 74: gb\_htg15:\*
- 75: gb\_htg16:\*
- 76: gb\_htg17:\*
- 77: gb\_htg18:\*
- 78: gb\_htg19:\*
- 79: gb\_htg20:\*
- 80: gb\_htg21:\*
- 81: gb\_htg22:\*
- 82: gb\_htg23:\*
- 83: gb\_htg24:\*
- 84: gb\_htg25:\*
- 85: gb\_pr1:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_ro1:\*
- 95: gb\_ro2:\*
- 96: gb\_in4:\*
- 97: gb\_pr10:\*
- 98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	321	100.0	321	9	AX060782 Sequence
2	318	99.1	321	9	AX060810 Sequence
3	268.2	83.6	321	9	AX060786 Sequence
4	249.6	77.8	321	94	MUSCMVF
5	249.6	77.8	321	94	MUSGKACV
6	249.6	77.8	370	94	MUSGKXD
7	248	77.3	321	94	AF163757
8	248	77.3	321	94	MUSCMVH

```

9      248      77.3      381      10      E07933      cDNA encodi
10     248      77.3      381      10      I31959      Sequence 82
11     248      77.3      381      10      I78571      Sequence 82
12     248      77.3      381      10      I78626      Sequence 82
13     248      77.3      431      94      MUSIGKCNJ      Mouse Ig re
14     246.4      76.8      324      94      AF139844      Mus muscu
15     246.4      76.8      324      94      AF139849      Mus muscu
16     246.4      76.8      330      94      MUSIGL2VK      Mus muscu
17     246.4      76.8      645      94      AB048528      Mus muscu
18     244.8      76.3      324      94      AF139845      Mus muscu
19     244.8      76.3      324      94      AF139846      Mus muscu
20     244.8      76.3      381      94      AF045514      Mus muscu
21     244.8      76.3      582      94      MM026998      Mus muscu
22     244.8      76.3      738      94      MM040581      Mus muscu
23     243.2      75.8      321      94      AF113242      Mus muscu
24     243.2      75.8      321      94      AF113243      Mus muscu
25     243.2      75.8      321      94      MM0277215      Mus muscu
26     243.2      75.8      321      94      MM0277216      Mus muscu
27     243.2      75.8      324      94      AF139847      Mus muscu
28     243.2      75.8      324      94      AF139848      Mus muscu
29     243.2      75.8      348      94      MMY16070      Mus muscu
30     242.8      75.6      324      94      MM060469      Mus muscu
31     241.6      75.3      324      94      AF087031      Mus muscu
32     241.6      75.3      420      94      MUSIGKCN      Mouse Ig ka
33     241.6      75.3      5238      9      A07699      Synthetic p
34     241      75.1      317      94      MMIGIKL4      Mouse mRNA
35     238.8      74.4      317      94      MUSIGVABU      Mouse mRNA
36     237.4      74.0      313      94      MUSIGVABU      Mouse mRNA
37     237      73.8      321      94      MMU16181      Mus muscu
38     236.8      73.8      381      94      MUSIGRAQA      Mus muscu
39     236.6      73.7      307      94      AF139235      Mus muscu
40     236.4      73.6      313      94      MUSIGVABW      Mus muscu
41     236      73.5      323      94      MUSANTDNF      Mus muscu
42     235.8      73.5      318      94      MMIGKVR4      Mouse anti-
43     235.6      73.4      306      94      MMIGLT91      Mouse immun
44     235.6      73.4      315      94      MM088691      Mus muscu
45     235.2      73.3      300      94      MUSIGRABJ      Mouse Ig ka
```

ALIGNMENTS

```

RESULT 1
AX060782      321 bp      DNA
LOCUS      Sequence 3 from Patent WO0078815.
DEFINITION
ACCESSION      AX060782
VERSION
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      synthetic construct.
REFERENCE      1 (bases 1 to 321)
AUTHORS      Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      encoding same and methods of use
JOURNAL      Patent: WO 0078815-A 3 28-DEC-2000;
JOURNAL      Applied Molecular Evolution (US)
FEATURES
source
1..321
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>321
/codon_start=1
/transl_table=11
/protein_id="CAC24889.1"
/db_xref="GI:12406163"
/translation="EIVLTQSPGATLSLSPGERATLSCQASQISNHLHWYQORPGQAP
RLIKYRSQISGIPARFSGSGDTFTLTISLEPEDFAVYICQSGSWPHTFGGT
KVEIK"
BASE COUNT      78 a      93 c      79 g      71 t
ORIGIN
```

```

Query Match      100.0%; Score 321; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.4e-90;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      GAGATTGTGCTAACTCAGTCTCCAGCCACCCTCTCTCTCAGCCAGGAGAAAGGGGACT 60
DB      1      GAGATTGTGCTAACTCAGTCTCCAGCCACCCTCTCTCTCAGCCAGGAGAAAGGGGACT 60

QY      61      CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
DB      61      CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120

QY      121      GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
DB      121      GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180

QY      181      AGTTTCAGTGGCAGTGGATGAGGAGGAGATTTCACCTCACTATCTCCAGTCTGGAGCCT 240
DB      181      AGTTTCAGTGGCAGTGGATGAGGAGGAGATTTCACCTCACTATCTCCAGTCTGGAGCCT 240

QY      241      GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGG 300
DB      241      GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGGAGG 300

QY      301      GGGACCAAGGTGGAATTAAG 321
DB      301      GGGACCAAGGTGGAATTAAG 321

RESULT 2
AX060810      321 bp      DNA
LOCUS      Sequence 31 from Patent WO0078815.
DEFINITION
ACCESSION      AX060810
VERSION
KEYWORDS      AX060810.1 GI:12406189
SOURCE      synthetic construct.
ORGANISM      synthetic construct.
REFERENCE      1 (bases 1 to 321)
AUTHORS      Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      encoding same and methods of use
JOURNAL      Patent: WO 0078815-A 31 28-DEC-2000;
JOURNAL      Applied Molecular Evolution (US)
FEATURES
source
1..321
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="grafted antibody variable region"
variation      145..147
/notes="NNN-CGT OR ATG"
BASE COUNT      76 a      93 c      78 g      71 t      3 others
ORIGIN

Query Match      99.1%; Score 318; DB 9; Length 321;
Best Local Similarity 99.1%; Pred. No. 4.8e-89;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1      GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
DB      1      GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60

QY      61      CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
DB      61      CTTTCTGCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120

QY      121      GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
DB      121      GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
```

QY 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240  
|||||  
Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240  
|||||  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
QY 301 GGGACCAAGTGGAAATTAAG 321  
|||||  
Db 301 GGGACCAAGTGGAAATTAAG 321  
|||||

RESULT 3  
AX060786 321 bp DNA PAT 22-JAN-2001  
LOCUS Sequence 7 from Patent WO0078815.  
DEFINITION AX060786  
ACCESSION AX060786  
VERSION AX060786.1 GI:12406166  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Huse,W.D. and Wu,H.  
TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 78-DEC-2000;  
Applied Molecular Evolution (US)  
FEATURES  
source  
1..321  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
CDS  
1..321  
<1..321  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC24891.1"  
/db\_xref="GI:12406167"  
/translations="DIVLTQSPATLSVTPGDVSVLSQASQSLNHLHWYQOKSHESP  
RLLIKYSQISGIPSRFSGSGTDFALINSVEYEDFGYFCQQSGSPHFVGGGT  
KLEIK"  
BASE COUNT 83 a 83 c 77 g 78 t  
ORIGIN  
Query Match 83.68; Score 268.2; DB 9; Length 321;  
Best Local Similarity 89.78; Pred. No. 2.1e-73;  
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGGACT 60  
|||||  
Db 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCCAGGAGATAGGTCAGT 60  
|||||  
QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
|||||  
Db 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
|||||  
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTATCGTTGGATCCCGCC 180  
|||||  
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCCAAGTATCGTTGGATCCCGTCC 180  
|||||  
QY 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240  
|||||  
Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCAACAGTGTGGAGACT 240  
|||||  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
QY 301 GGGACCAAGTGGAAATTAAG 321  
|||||

QY 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240  
|||||  
Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCAACAGTGTGGAGACT 240  
|||||  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
QY 301 GGGACCAAGTGGAAATTAAG 321  
|||||

Db 301 GGGACCAAGTGGAAATTAAG 321  
|||||

RESULT 4  
MUSCMVF 321 bp mRNA ROD 26-JUL-1993  
LOCUS Mouse mRNA sequence, partial cds.  
DEFINITION M95943  
ACCESSION M95943  
VERSION M95943.1 GI:309175  
KEYWORDS  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Simpson,J.A., Chow,J.C., Baker,J., Avdaloovic,N.M., Yuan,S.,  
Co.W.S., Vasquez,M., Britt,W.J. and Coellingh,K.L.  
TITLE Untitled  
JOURNAL Unpublished (1992)  
FEATURES  
source  
1..321  
/organism="Mus musculus"  
/strain="BALB/c"  
/sub\_species="domesticus"  
/db\_xref="taxon:10090"  
/cell\_line="MAB 33"  
/cell\_type="hybridoma"  
mat\_peptide 1..321  
/note="putative"  
BASE COUNT 86 a 81 c 74 g 80 t  
ORIGIN  
Query Match 77.89; Score 249.6; DB 94; Length 321;  
Best Local Similarity 86.28; Pred. No. 1.4e-67;  
Matches 276; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGGACT 60  
|||||  
Db 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGGTCAGT 60  
|||||  
QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
|||||  
Db 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
|||||  
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTATCGTTGGATCCCGCC 180  
|||||  
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCCAAGTATCGTTGGATCCCGTCC 180  
|||||  
QY 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240  
|||||  
Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTCACCTCTCACTATCAACAGTGTGGAGACT 240  
|||||  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGCAGTTCGGAGGG 300  
|||||  
QY 301 GGGACCAAGTGGAAATTAAG 320  
|||||  
Db 301 GGGACCAAGTGGAAATTAAG 320  
|||||

RESULT 5  
MUSIGKACY 321 bp mRNA ROD 27-APR-1993  
LOCUS Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region  
DEFINITION M35667  
ACCESSION M35667  
VERSION M35667.1 GI:196584  
KEYWORDS immunoglobulin light chain; immunoglobulin-kappa; processed gene;  
variable region VK23.  
SOURCE Mouse hybridoma, cDNA to mRNA, clone 10K-106.  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and  
Brooks, W.B.R.  
TITLE A three-dimensional model of an anti-lysozyme antibody  
JOURNAL J. Mol. Biol. 194, 713-724 (1987)  
MEDLINE 88011212  
FEATURES Location/Qualifiers

Source  
1..321  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
<1..>321  
/note="lysozyme binding Ig kappa chain V23-J2 region"  
/codon\_start=1  
/protein\_id="AAA38741.1"  
/db\_xref="GI:196585"  
/translation="DIVLTQSPATLSVTPGNSVLSQRSQSISGNLHWYQKSHESP  
RLIIRYASQISGIPSRFSGSGDTFLINSVETEDFGMYFCQCSNWPYFGGGT  
KLEIK"

BASE COUNT 88 a 80 c 75 g 78 t  
ORIGIN

Query Match 77.8%; Score 249.6; DB 94; Length 321;  
Best Local Similarity 86.2%; Pred. No. 1.4e-67;  
Matches 276; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 GAGATTGCTTAAGTCTCAGCCAGCCCTCTCTCAGCCAGGAGGAGGCGACT 60  
|||  
Db 1 GATATTGCTTAAGTCTCAGCCAGCCCTCTCTCAGCCAGGAGGAGGCGACT 60  
QY 61 CTTCCTGCGAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
|||  
Db 61 CTTCCTGCGAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180  
|||  
Db 121 CATGAGTCTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180  
QY 181 AGGTTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 240  
|||  
Db 181 AGGTTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 240  
QY 241 GAAGATTTTGGAGTATTTCTCTCAACAGAGTGCGGAGGAGGAGGAGGAGGAGG 300  
|||  
Db 241 GAAGATTTTGGAGTATTTCTCTCAACAGAGTGCGGAGGAGGAGGAGGAGGAGG 300  
QY 301 GGGACCAAGGTGGAATATA 320  
|||  
Db 301 GGGACCAAGGTGGAATATA 320

RESULT 6  
MUSIGKXD MUSTGKXD 370 bp mRNA ROD 27-APR-1993  
LOCUS Mouse Ig active kappa-chain V-region, partial cds.  
DEFINITION M93959  
ACCESSION M93959  
VERSION M93959.1 GI:197572  
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;  
processed gene.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 370)  
AUTHORS Takeda, F., Wise, K.S. and Hoffman, R.W.  
TITLE Nucleotide sequences of immunoglobulin heavy and light chain  
V-regions from a monoclonal autoantibody specific for a unique set  
of small nuclear ribonucleoprotein complexes  
JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)  
MEDLINE 92375706  
FEATURES Location/Qualifiers

Source  
1..370  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/map="6"  
1..370  
/gene="IgK"  
/partial  
/note="putative"  
/codon\_start=1  
/function="variable region"  
/product="immunoglobulin kappa-chain"  
/protein\_id="AAA39079.1"  
/db\_xref="GI:554148"  
/translation="GLMLFWISASRGDILVLTQSPATLSVTPGDKVLSQRSQSISNY  
LHWYQKSHESPRLIIRYASQISGIPSRFSGSGDTFLINSVETEDFGMYFCQQ  
SNWPHTTSGTGLKIKRADA"  
BASE COUNT 96 a 90 c 86 g 98 t  
ORIGIN

Query Match 77.8%; Score 249.6; DB 94; Length 370;  
Best Local Similarity 86.2%; Pred. No. 1.4e-67;  
Matches 276; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 GAGATTGCTTAAGTCTCAGCCAGCCCTCTCTCAGCCAGGAGGAGGCGACT 60  
|||  
Db 37 GATATTGCTTAAGTCTCAGCCAGCCCTCTCTCAGCCAGGAGGAGGCGACT 96  
QY 61 CTTCCTGCGAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
|||  
Db 97 CTTCCTGCGAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 156  
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180  
|||  
Db 157 CATGAGTCTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 216  
QY 181 AGGTTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 240  
|||  
Db 217 AGGTTCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGCC 276  
QY 241 GAAGATTTTGGAGTATTTCTCTCAACAGAGTGCGGAGGAGGAGGAGGAGGAGG 300  
|||  
Db 277 GAAGATTTTGGAGTATTTCTCTCAACAGAGTGCGGAGGAGGAGGAGGAGGAGG 336  
QY 301 GGGACCAAGGTGGAATATA 320  
|||  
Db 337 GGGACCAAGGTGGAATATA 356

RESULT 7  
AF163757 AF163757 321 bp mRNA ROD 04-AUG-1999  
LOCUS Mus musculus mab 101.4.1 immunoglobulin light chain variable region  
DEFINITION mRNA, partial cds.  
ACCESSION AF163757  
VERSION AF163757.1 GI:5690320  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.  
TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal  
Mouse Monoclonal Antibodies  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 321)  
AUTHORS Mertens, N.M. and Cunningham, M.W.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma  
University Health Sciences Center, 940 St. Young Blvd, Oklahoma

```
FEATURES
source
    City, OK 73190, USA
    Location/Qualifiers
    1..321
    /organism="Mus musculus"
    /strain="BALB/c"
    /db_xref="taxon:10090"
    /note="mab 101.4.1"
    <1..>321
    /codon_start=1
    /product="immunoglobulin light chain variable region"
    /protein_id="AA047036.1"
    /db_xref="GI:5690321"
    /translation="DIVLTQSPATLSVTPGDSSVLSQRSQSSNNLHWYQQRKSHESP
    RLKIKVASQISGIPSRFSGSGDTFTLSINSVETDFMGYFCQGSNSWPLTFGAGT
    KLELK"
BASE COUNT      83 a      83 c      73 g      82 t
ORIGIN
    Query Match      77.3%; Score 248; DB 94; Length 321;
    Best Local Similarity 85.9%; Pred. No. 4.6e-67;
    Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGTCCGGGAGATAGCGTCAGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CTTTCCTGCCAGGCGCCGCAAAAGTATTAGCAACACCTACACTGCTGTATCAACAAGGCGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CTTTCCTGCCAGGCGCCGCAAAAGTATTAGCAACACCTACACTGCTGTATCAACAATCA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GGTCAGCCCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCCGCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCCGCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCACCTCAGTATCTCCAGTCTGGAGCCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCACCTCAGTATCTCCAGTCTGGAGCCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GGGACCAAGTGGAAATTA 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GGGACCAAGTGGAAATTA 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
MUSCMVH      321 bp      mRNA      ROD      26-JUL-1993
LOCUS
DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95945
VERSION M95945.1 GI:309177
KEYWORDS Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
SOURCE
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 321)
REFERENCE
    Simpson,J.A., Chow,J.C., Baker,J., Avdlovic,N.M., Yuan,S.,
    Co,M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L.
    Co,M.S., Vasquez,M., Britt,W.J. and Coelingh,K.L.
TITLE
    Untitled
JOURNAL
    Unpublished (1992)
FEATURES
source
    Location/Qualifiers
    1..321
    /organism="Mus musculus"
    /strain="BALB/c"
    /sub_species="domesticus"
    /db_xref="taxon:10090"
    /cell_line="MAB 5"
    /cell_type="hybridoma"
    1..321
    mat_peptide
```

```
BASE COUNT      85 a      79 c      77 g      80 t
ORIGIN
    Query Match      77.3%; Score 248; DB 94; Length 321;
    Best Local Similarity 85.9%; Pred. No. 4.6e-67;
    Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGTCCGGGAGATAGCGTCAGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CTTTCCTGCCAGGCGCCGCAAAAGTATTAGCAACACCTACACTGCTGTATCAACAAGGCGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CTTTCCTGCCAGGCGCCGCAAAAGTATTAGCAACACCTACACTGCTGTATCAACAATCA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GGTCAGCCCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCCGCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCCGCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCACCTCAGTATCTCCAGTCTGGAGCCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCACCTCAGTATCTCCAGTCTGGAGCCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GGGACCAAGTGGAAATTA 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GGGACCAAGTGGAAATTA 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
E07933
LOCUS
DEFINITION cDNA encoding variable region of mouse anti-PHV-1 antibody L chain.
ACCESSION E07933
VERSION E07933.1 GI:2176065
KEYWORDS JP 1994217786-A/2.
SOURCE
ORGANISM
    Mus sp.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 381)
REFERENCE
    Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y.
    Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y.
TITLE
    ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT
    ENCODING THE SAME ANTIBODY
JOURNAL
    Patent: JP 1994217786-A 2 09-AUG-1994;
    CHERO SERO THERAPEUT RES INST
COMMENT
    OS Mus sp. (mouse)
    PN JP 1994217786-A/2
    PD 09-AUG-1994
    PF 28-NOV-1992 JP 1992341255
    PI KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO, PI
    TOKIYOSHI YUKIO
    PC C12P21/08.A61K39/395.C07K15/00.C12N15/13.(C12P21/08.C12R1:91);
    CC strandedness: Double;
    CC topology: Linear;
    CC hypothetical: No;
    CC anti-sense: No;
    FH Key
    FH Location/Qualifiers
    1..381
    /organism="Mus sp."
    FT mat_peptide
    1..381
    /product="variable region of mouse anti-PHV-1
    antibody L
    chain".
    FT Location/Qualifiers
    1..381
    /organism="Mus sp."
    FT source
```

```
/db_xref="taxon:10095"
BASE COUNT      94 a      98 c      86 g      103 t
ORIGIN

Query Match      77.3%; Score 248; DB 10; Length 381;
Best Local Similarity 85.9%; Pred. No. 4.6e-67;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGGGCGACT 60
Db 61 GATATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTGCTGACTCCAGGAGATAGCGTCACT 120
QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGGCGCT 120
Db 121 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGTCA 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCCATCTCTGGGATCCCGGCC 180
Db 181 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGGCTCCCATCTCTGGGATCCCGGCC 240
QY 181 AGTTTCTGCGAGTCTCATCAAGTATCGTTCAGGCTCCCATCTCTGGGATCCCGGCC 300
Db 301 GAGATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGGGCGACT 360
QY 301 GGGACCAAGGTGGAATAA 320
Db 361 GGGACCAAGGTGGAATAA 380

RESULT 10
LOCUS      I31959      381 bp      DNA      PAT      06-FEB-1997
DEFINITION Sequence 82 from patent US 5585089.
ACCESSION I31959
VERSION I31959.1 GI:1822750
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 381)
AUTHORS Queen,C.L. and Selick,H.E.
TITLE Humanized immunoglobulins
JOURNAL Patent: US 5585089-A 82 17-DEC-1996;
FEATURES Location/Qualifiers
source 1..381
BASE COUNT 97 a 92 c 89 g 103 t
ORIGIN

Query Match      77.3%; Score 248; DB 10; Length 381;
Best Local Similarity 85.9%; Pred. No. 4.6e-67;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGGGCGACT 60
Db 61 GATATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTGCTGACTCCAGGAGATAGCGTCACT 120
QY 61 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGGCGCT 120
Db 121 CTTTCTGCGAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAGTCA 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCAGGCTCCCATCTCTGGGATCCCGGCC 180
Db 181 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGGCTCCCATCTCTGGGATCCCGGCC 240
QY 181 AGTTTCTGCGAGTCTCATCAAGTATCGTTCAGGCTCCCATCTCTGGGATCCCGGCC 300
Db 301 GAGATTGCTGCTACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGGGCGACT 360
QY 301 GGGACCAAGGTGGAATAA 320
Db 361 GGGACCAAGGTGGAATAA 380

RESULT 12
LOCUS      I78626      381 bp      DNA      PAT      03-APR-1998
DEFINITION Sequence 82 from patent US 5693762.
ACCESSION I78626
VERSION I78626.1 GI:3014780
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 381)
AUTHORS Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelingh,K.L.
```



```
SP2/0"
/tissue_type="spleen"
<1..>324
/gene="IgG"
/notes="variable region (VJ)"
CDS
<1..>324
/gene="IgG"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
Vk23"
/protein_id="AAD28631.1"
/db_xref="GI:4732153"
/translation="DIVLTQSPATLSVTPGESVLSCRASQSISSLNLHFWFOOKSHESP
RLIKYASLSIGIPSRFGSGDTFLINSVETEDFGMYFCQSDNWPHTFGSGT
KLEIKR"
misc_feature
70..105
/gene="IgG"
/notes="CDR1; complementarity determining region 1"
misc_feature
148..168
/gene="IgG"
/notes="CDR2; complementarity determining region 2"
misc_feature
265..291
/gene="IgG"
/notes="CDR3; complementarity determining region 3"
J_segment
287..324
/gene="IgG"
/notes="Jk2"
BASE COUNT      88 a      82 c      72 g      82 t
ORIGIN
Query Match      76.8%; Score 246.4; DB 94; Length 324;
Best Local Similarity 85.6%; Pred. No. 1.5e-66;
Matches 274; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GAGATTGCTCACTCAGTCCAGCCACCCCTGTCTCTCAGCCAGGAAAGGCGCT 60
Db 1 GATATTGCTCACTCAGTCCAGCCACCCCTGTCTCTCAGCCAGGAAAGGCGCT 60
QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACTACACTGTGTATCAACAAAGGCT 120
Db 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACTACACTGTGTATCAACAAAGGCT 120
QY 121 GGTCAAGCCCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 121 GGTCAAGCCCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
QY 121 CATGAGTCTCCAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 121 CATGAGTCTCCAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
QY 181 AGGTTCAATGGCAGTGGATCAGGAGACAGATTTCACCTCTCAGTATCAACAGTGTGGAGCT 240
Db 181 AGGTTCAATGGCAGTGGATCAGGAGACAGATTTCACCTCTCAGTATCAACAGTGTGGAGCT 240
QY 241 GAAGATTTTGGAGTATTAATGATCAACAGAGTGGCAGTGGCCTCACACCTTCGGAGGG 300
Db 241 GAAGATTTTGGAGTATTAATGATCAACAGAGTGGCAGTGGCCTCACACCTTCGGAGGG 300
RESULT 15
AF139849
LOCUS
DEFINITION Mus musculus clone 38 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
ACCESSION AF139849
VERSION AF139849.1 GI:4732162
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
JOURNAL 99406777
MEDLINE 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source
1..324
Location/Qualifiers
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/chromosome="6"
/clone="38"
/cell_type="B cell hybridoma (spontaneous fusion with
SP2/0)"
/tissue_type="spleen"
<1..>324
/gene="IgG"
/notes="variable region (VJ)"
<1..>324
/gene="IgG"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
Vk23"
/protein_id="AAD28636.1"
/db_xref="GI:4732163"
/translation="DIVLTQSPATLSVTPGDSVLSCRASQSISSLNLHFWFOOKSHESP
RLIKYASQISIGIPSRFNGSGDTFLINSVETEDFGMYFCQSDNWPHTFGSGT
KLEIKR"
misc_feature
70..105
/gene="IgG"
/notes="CDR1; complementarity determining region 1"
misc_feature
148..168
/gene="IgG"
/notes="CDR2; complementarity determining region 2"
misc_feature
265..291
/gene="IgG"
/notes="CDR3; complementarity determining region 3"
J_segment
287..324
/gene="IgG"
/notes="Jk2"
BASE COUNT      87 a      82 c      74 g      81 t
ORIGIN
Query Match      76.8%; Score 246.4; DB 94; Length 324;
Best Local Similarity 85.6%; Pred. No. 1.5e-66;
Matches 274; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GAGATTGCTCACTCAGTCCAGCCACCCCTGTCTCTCAGCCAGGAAAGGCGCT 60
Db 1 GATATTGCTCACTCAGTCCAGCCACCCCTGTCTCTCAGCCAGGATAGCGTCAGT 60
QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACTACACTGTGTATCAACAAAGGCT 120
Db 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCACTACACTGTGTATCAACAAAGGCT 120
QY 121 GGTCAAGCCCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 121 GGTCAAGCCCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
QY 121 CATGAGTCTCCAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
Db 121 CATGAGTCTCCAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGGCC 180
QY 181 AGGTTCAATGGCAGTGGATCAGGAGACAGATTTCACCTCTCAGTATCAACAGTGTGGAGCT 240
Db 181 AGGTTCAATGGCAGTGGATCAGGAGACAGATTTCACCTCTCAGTATCAACAGTGTGGAGCT 240
QY 241 GAAGATTTTGGAGTATTAATGATCAACAGAGTGGCAGTGGCCTCACACCTTCGGAGGG 300
Db 241 GAAGATTTTGGAGTATTAATGATCAACAGAGTGGCAGTGGCCTCACACCTTCGGAGGG 300
```



Qy 301 GGGACCAAGGTGGAATTA 320  
||||||| ||||| ||  
Db 301 GGGACCAAGGTGGAATTA 320

Search completed: October 11, 2001, 15:09:31  
Job time: 6353 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 14:33:59 ; Search time 2341.88 Seconds  
(without alignments)  
1295.697 Million cell updates/sec

Title: US-08-791-391A-3  
Perfect score: 321  
Sequence: 1 GAGATTGCTGTAACAGTC.....GGACCAAGGTGGAATTAAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues 20456230  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_est3:*
4:	gb_est4:*
5:	gb_est5:*
6:	gb_est6:*
7:	gb_est7:*
8:	gb_est8:*
9:	gb_est9:*
10:	gb_est10:*
11:	gb_est11:*
12:	gb_est12:*
13:	gb_est13:*
14:	gb_est14:*
15:	gb_est15:*
16:	gb_est16:*
17:	gb_est17:*
18:	gb_est18:*
19:	gb_est19:*
20:	gb_est20:*
21:	gb_est21:*
22:	gb_est22:*
23:	gb_est23:*
24:	gb_est24:*
25:	gb_est25:*
26:	gb_est26:*
27:	gb_est27:*
28:	gb_est28:*
29:	gb_est29:*
30:	gb_est30:*
31:	gb_est31:*
32:	gb_est32:*
33:	gb_est33:*
34:	gb_est34:*
35:	gb_est35:*
36:	gb_est36:*
37:	gb_est37:*
38:	gb_est38:*
39:	gb_est39:*
40:	gb_est40:*
41:	gb_est41:*
42:	gb_est42:*
43:	gb_est43:*
44:	gb_est44:*
45:	gb_est45:*
46:	gb_est46:*
47:	gb_est47:*
48:	gb_est48:*
49:	gb_est49:*
50:	gb_est50:*
51:	gb_est51:*
52:	gb_est52:*
53:	gb_est53:*
54:	gb_est54:*
55:	gb_est55:*
56:	gb_est56:*
57:	gb_est57:*
58:	gb_est58:*
59:	gb_est59:*
60:	gb_est60:*
61:	gb_est61:*
62:	gb_est62:*
63:	gb_est63:*
64:	gb_est64:*
65:	gb_est65:*
66:	gb_est66:*
67:	gb_est67:*
68:	gb_est68:*
69:	gb_est69:*
70:	gb_est70:*
71:	gb_est71:*
72:	gb_est72:*
73:	gb_est73:*
74:	gb_est74:*
75:	gb_est75:*
76:	gb_est76:*
77:	gb_est77:*
78:	gb_est78:*
79:	gb_est79:*
80:	gb_est80:*
81:	gb_est81:*
82:	gb_est82:*
83:	gb_est83:*
84:	gb_est84:*
85:	gb_est85:*
86:	gb_est86:*
87:	gb_est87:*
88:	gb_est88:*
89:	gb_est89:*
90:	gb_est90:*
91:	gb_est91:*
92:	gb_est92:*
93:	gb_est93:*
94:	gb_est94:*
95:	gb_est95:*
96:	gb_est96:*
97:	gb_est97:*
98:	gb_est98:*
99:	gb_est99:*
100:	gb_est100:*
101:	gb_est101:*
102:	gb_est102:*
103:	gb_est103:*
104:	gb_est104:*
105:	gb_est105:*
106:	gb_est106:*
107:	gb_est107:*
108:	gb_est108:*
109:	gb_est109:*
110:	gb_est110:*
111:	gb_est111:*
112:	gb_est112:*
113:	gb_est113:*
114:	gb_est114:*
115:	gb_est115:*
116:	gb_est116:*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est67:\*  
137: gb\_est68:\*  
138: gb\_est69:\*  
139: gb\_est70:\*  
140: gb\_est71:\*  
141: gb\_est72:\*  
142: gb\_est73:\*  
143: gb\_est74:\*  
144: gb\_est75:\*  
145: gb\_est76:\*  
146: gb\_est77:\*  
147: gb\_est78:\*  
148: gb\_est79:\*  
149: gb\_est80:\*  
150: gb\_est81:\*  
151: gb\_est82:\*  
152: gb\_est83:\*  
153: gb\_est84:\*  
154: gb\_est85:\*  
155: gb\_est86:\*  
156: gb\_est87:\*  
157: gb\_est88:\*  
158: gb\_est89:\*  
159: gb\_est90:\*  
160: gb\_est91:\*  
161: gb\_est92:\*  
162: gb\_est93:\*  
163: gb\_est94:\*  
164: gb\_est95:\*  
165: gb\_est96:\*  
166: gb\_est97:\*  
167: gb\_est98:\*  
168: gb\_est99:\*  
169: gb\_est100:\*  
170: gb\_est101:\*  
171: gb\_est102:\*  
172: gb\_est103:\*  
173: gb\_est104:\*  
174: gb\_est105:\*  
175: gb\_est106:\*  
176: gb\_est107:\*  
177: gb\_est108:\*  
178: gb\_est109:\*  
179: gb\_est110:\*  
180: gb\_est111:\*  
181: gb\_est112:\*  
182: gb\_est113:\*  
183: gb\_est114:\*  
184: gb\_est115:\*  
185: gb\_est116:\*  
186: gb\_est117:\*  
187: gb\_est118:\*  
188: gb\_est119:\*  
189: gb\_est120:\*

190: gb\_est121:\*  
191: gb\_est122:\*  
192: gb\_est123:\*  
193: gb\_est124:\*  
194: gb\_est125:\*  
195: gb\_est126:\*  
196: gb\_est127:\*  
197: gb\_est128:\*  
198: gb\_est129:\*  
199: gb\_est130:\*  
200: gb\_est131:\*  
201: gb\_est132:\*  
202: gb\_est133:\*  
203: gb\_est134:\*  
204: gb\_est135:\*  
205: gb\_est136:\*  
206: gb\_est137:\*  
207: gb\_est138:\*  
208: gb\_est139:\*  
209: gb\_est140:\*  
210: gb\_est141:\*  
211: gb\_est142:\*  
212: gb\_est143:\*  
213: gb\_est144:\*  
214: gb\_est145:\*  
215: gb\_est146:\*  
216: gb\_est147:\*  
217: gb\_est148:\*  
218: gb\_est149:\*  
219: gb\_est150:\*  
220: gb\_est151:\*  
221: gb\_est152:\*  
222: gb\_est153:\*  
223: gb\_est154:\*  
224: gb\_est155:\*  
225: gb\_est156:\*  
226: gb\_est157:\*  
227: gb\_est158:\*  
228: gb\_est159:\*  
229: gb\_est160:\*  
230: gb\_est161:\*  
231: gb\_est162:\*  
232: gb\_est163:\*  
233: gb\_est164:\*  
234: gb\_est165:\*  
235: gb\_est166:\*  
236: gb\_est167:\*  
237: gb\_est168:\*  
238: gb\_est169:\*  
239: gb\_est170:\*  
240: gb\_est171:\*  
241: gb\_est172:\*  
242: gb\_est173:\*  
243: gb\_est174:\*  
244: gb\_est175:\*  
245: gb\_est176:\*  
246: gb\_est177:\*  
247: gb\_est178:\*  
248: gb\_est179:\*  
249: gb\_est180:\*  
250: gb\_est181:\*  
251: gb\_est182:\*  
252: gb\_est183:\*  
253: gb\_est184:\*  
254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	219.6	68.4	738	150	BF582153	BF582153 602099743
2	214	66.7	949	150	BF579007	BF579007 602096124
3	206.4	64.3	946	155	BG569760	BG569760 602590367
4	206	64.2	434	115	AW406486	AW406486 UI-HF-BLO
5	203.2	63.3	398	115	AW405309	AW405309 UI-HF-BLO
6	201.6	62.8	482	32	AV733856	AV733856 AV733856
7	201.6	62.8	519	115	AW405183	AW405183 UI-HF-BLO
8	201.6	62.8	624	166	BG306691	BG306691 601104076
9	201.2	62.7	385	115	AW405025	AW405025 UI-HF-BLO
10	200	62.3	468	115	AW405643	AW405643 UI-HF-BLO
11	198.4	61.8	468	115	AW405406	AW405406 UI-HF-BLO
12	198.4	61.8	1015	155	BG536848	BG536848 602566386
13	196.8	61.3	465	115	AW404697	AW404697 UI-HF-BLO
14	195.8	61.0	548	155	BG560486	BG560486 602587455
15	193.6	60.3	485	110	AV734882	AV734882 AV734882
16	193.4	60.2	451	170	BF874574	BF874574 IL3-PT011
17	193.4	60.2	758	154	BG534598	BG534598 602553450
18	192	59.8	514	115	AW405207	AW405207 UI-HF-BLO
19	192	59.8	615	122	AW959456	AW959456 EST371526
20	191.8	59.8	461	115	AW406219	AW406219 UI-HF-BLO
21	191.8	59.8	849	150	BF583521	BF583521 602101553
22	191.8	59.8	1061	151	BF663663	BF663663 602145371
23	190.8	59.4	330	115	AW400212	AW400212 UI-HF-BLO
24	189.8	59.1	413	115	AW406440	AW406440 UI-HF-BLO
25	189.6	59.1	656	154	BG482934	BG482934 602502942
26	188.8	58.8	409	115	AW406057	AW406057 UI-HF-BLO
27	188	58.6	639	32	AV734416	AV734416 AV734416
28	188	58.6	708	166	BF309445	BF309445 601095331
29	187.2	58.3	443	115	AW403460	AW403460 UI-HF-BLO
30	187.2	58.3	448	115	AW404726	AW404726 UI-HF-BLO
31	186.2	58.0	868	155	BG539952	BG539952 602567464
32	185.8	57.9	317	115	AW404261	AW404261 UI-HF-BLO
33	185.6	57.8	748	154	BG529887	BG529887 602558987
34	185.4	57.8	504	115	AW405787	AW405787 UI-HF-BLO
35	183.8	57.3	369	115	AW405943	AW405943 UI-HF-BLO
36	183	57.0	833	172	BF972335	BF972335 602244740
37	182.8	56.9	473	115	AW406934	AW406934 UI-HF-BLO
38	182.2	56.8	518	115	AW406576	AW406576 UI-HF-BLO
39	182.2	56.8	644	115	AW405817	AW405817 UI-HF-BLO
40	182.2	56.8	719	154	BG536027	BG536027 602564303
41	182	56.7	895	151	BF663197	BF663197 602144313
42	181.2	56.4	1047	155	BG545546	BG545546 602572793
43	180.8	56.3	425	115	AW406785	AW406785 UI-HF-BLO
44	179	55.8	395	122	AW951626	AW951626 EST363711
45	179	55.8	408	115	AW404674	AW404674 UI-HF-BLO

## ALIGNMENTS

RESULT 1  
 BF582153  
 LOCUS  
 DEFINITION  
 738 bp mRNA  
 602099743F1 NCI\_CGAP\_C024 Mus musculus cDNA clone IMAGE:4219402 5',  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 738)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9801 row: f column: 11  
High quality sequence stop: 714.  
Location/Qualifiers  
1. 738  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4219402"  
/clone.lib="NCI CGAP Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: pcMV-SPOrt6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library."

BASE COUNT	210 a	189 c	172 g	167 t	
ORIGIN					
Query Match	68.4%;	Score 219.6;	DB 150;	Length 738;	
Best Local Similarity	84.9%;	Pred. No. 1.4e-57;			
Matches 270;	Conservative 0;	Mismatches 44;	Indels 4;	Gaps 2;	
QY	6	TGTGCTAACTCAGTCTCCAGCCACCCGTGTCTCTCAGCCAGGAGAAAGGCGACTCTTTTC	65		
Db	78	TGTGCTAACTCAGTCTCCAGCCACCCGTGTCTGTGACTCCAGGAGATAGCGTCAGCTCTTC	137		
QY	66	CTGCCAGGCCAGCAAAAGTATTAGCACACCCTACACTGGTATATCAACAAGGCCCTGGTCA	125		
Db	138	CTGCAGGGCCAGCCAAAAGTATTAGCACACACCTACACTGGTATATCAACAAAATCACATGA	197		
QY	126	AGCCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCACTCTCTGGGATCCCGCCAGGTT	185		
Db	198	GTCTCCAAGGCTTCTCATCAAGTATGCTTCCCAGTCCATCTCTGGGATCCCGTCCAGGTT	257		
QY	186	CAGTGGCAGTGGATCAGGGACAGATTTTCACCTCAGTATCTCCAGTCTGGAGCCTGAAGA	245		
Db	258	CAGTGGCAGTGGATCAGGGACAGATTTTCAGTCTCAGTATCAACAGTCTGGAGACTGAAGA	317		
QY	246	TTTTGTCAGTCTATTACTGTCTAACAGATGGCGAGTGGCCCTCA---CACGTTCCGGAGGGG	302		
Db	318	-TTTGGATGTATTCTTGTCACAGAGTAACAGCTGGCCTCAGCTCAGGTCGGTCTGG	376		
QY	303	GACCAAGGTGGAAATTAA	320		
Db	377	GACCAAGCTGGAGCTGAA	394		

RESULT	2				
LOCUS	BF579007				
DEFINITION	BF579007 949 bp mRNA EST		12-DEC-2000		
	602096124F1 NCT_CGAP_C024 Mus musculus cDNA clone IMAGE:4216180 5',				
	mRNA sequence.				
ACCESSION	BF579007				
VERSION	BF579007.1	GI:11652719			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 949)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>				



**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbbrp/image/image.html](http://www-bio.llnl.gov/dbbrp/image/image.html)  
Seq primer: M13 Forward.

```

FEATURES
source
Location/Qualifiers
1. 434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3060238"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: pf7x3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
99 a 127 c 106 g 102 t
BASE COUNT
ORIGIN

```

Query Match	64.28;	Score 206;	DB 115;	Length 434;
Best Local Similarity	78.08;	Pred. No. 2.le-53;		
Matches 248;	Conservative 0;	Mismatches 70;	Indels 0;	Gaps 0;
QY	3	GATTGTGCTAACTCAGTCCTCAGCCACCCCTGCTCTCTCAGCCCGAGGAGAAAGGGCGACTCT	62	
Db	7	GGTGTGTTGACACAGTCTCCAGCCACCCCTGTCTTTGTCTCCAGGGAGAGACCCACCT	66	
QY	63	TTCTTGCCAGGCCAGGCCAAAGTATTAGCAACCACTACACTGCTATCAACAAGAGCCCTGG	122	
Db	67	CTCTGCGAGGCCAGTCAGAGTATTAACAACACTACTAGCCCTGGTACCAACAGAAACCTGG	126	
QY	123	TCAAGCCCCAAGGTTCTTCATCAAGTATGCTTCCAGTGCATCTCTGGGATCCCGCCGAG	182	
Db	127	CCAGGCTCCCAGGGCTCCTCATCTATGATGATCCAAAGGGGCCACTGCGCATCCCGACGAG	186	
QY	183	GTTCAAGTGGCAGTGGATCGAGGACAGATTTACCCCTCAGTATCTCCAGTCTGGAGCCCTGA	242	
Db	187	GTTCAAGTGGCAGTGGGTCTGGGACAGACTTACATCTCACCATCAGACGCTTCGAGCCCTGA	246	
QY	243	AGATTTTTCAGTCTATTACTGCTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGGAGGGGG	302	
Db	247	AGATTTTTCGAATTATTACTGCTCAGACGCTAGCATCTGGCCACTCACTTTCGCGCGGAGG	306	
QY	303	GACCAAGGTGGAATTTAA	320	
Db	307	GACCAAGGTGGAGATCAA	324	

RESULT	5	
AW405309		
LOCUS		
DEFINITION		
AW405309	398 bp	mRNA
AW405309	UI-HP-BL0-ack-c-01-0-UI.r1	NIH_MGC_37 Homo sapiens cDNA clone
AW405309	IMAGE:3059305	5', mRNA sequence.
AW405309	1	GI:6924366
AW405309		EST.
AW405309		human.
ORGANISM		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	...	...	...	...
2	...	...	...	...
3	...	...	...	...
4	...	...	...	...
5	...	...	...	...
6	...	...	...	...
7	...	...	...	...
8	...	...	...	...
9	...	...	...	...
10	...	...	...	...
11	...	...	...	...
12	...	...	...	...
13	...	...	...	...
14	...	...	...	...
15	...	...	...	...
16	...	...	...	...
17	...	...	...	...
18	...	...	...	...
19	...	...	...	...
20	...	...	...	...
21	...	...	...	...
22	...	...	...	...
23	...	...	...	...
24	...	...	...	...
25	...	...	...	...
26	...	...	...	...
27	...	...	...	...
28	...	...	...	...
29	...	...	...	...
30	...	...	...	...
31	...	...	...	...
32	...	...	...	...
33	...	...	...	...
34	...	...	...	...
35	...	...	...	...
36	...	...	...	...
37	...	...	...	...
38	...	...	...	...
39	...	...	...	...
40	...	...	...	...
41	...	...	...	...
42	...	...	...	...
43	...	...	...	...
44	...	...	...	...
45	...	...	...	...
46	...	...	...	...
47	...	...	...	...
48	...	...	...	...
49	...	...	...	...
50	...	...	...	...
51	...	...	...	...
52	...	...	...	...
53	...	...	...	...
54	...	...	...	...
55	...	...	...	...
56	...	...	...	...
57	...	...	...	...
58	...	...	...	...
59	...	...	...	...
60	...	...	...	...
61	...	...	...	...
62	...	...	...	...
63	...	...	...	...
64	...	...	...	...
65	...	...	...	...
66	...	...	...	...
67	...	...	...	...
68	...	...	...	...
69	...	...	...	...
70	...	...	...	...
71	...	...	...	...
72	...	...	...	...
73	...	...	...	...
74	...	...	...	...
75	...	...	...	...
76	...	...	...	...
77	...	...	...	...
78	...	...	...	...
79	...	...	...	...
80	...	...	...	...
81	...	...	...	...
82	...	...	...	...
83	...	...	...	...
84	...	...	...	...
85	...	...	...	...
86	...	...	...	...
87	...	...	...	...
88	...	...	...	...
89	...	...	...	...
90	...	...	...	...
91	...	...	...	...
92	...	...	...	...
93	...	...	...	...
94	...	...	...	...
95	...	...	...	...
96	...	...	...	...
97	...	...	...	...
98	...	...	...	...
99	...	...	...	...
100	...	...	...	...

1 (bases 1 to 398)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Eco RI site shown at the beginning of the sequence.  
 Tissue procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://bio-llnl.gov/bbbr/image/image.html>  
 Seq. primer: M13 Forward.

FEATURES  
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3059305"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
88 a 123 c 98 g 89 t

```

BASE COUNT	88 a	123 c	98 g	89 t
ORIGIN				

```
Query Match      63.3%; Score 203.2; DB 115; Length 398;
Best Local Similarity 77.2%; Pred. No. 1.5e-52;
Matches 247; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
```

QY	1	GAGATTGCTAACTCAGTCTCAGCCACCCTGCTCTCAGCCACAGAGAAAGGGCAGCT	60
Db	44	GAATTTTCTTTGACACAGTCTCAGCCACCCTGCTTTGCTCCAGGGAAAGAGCCACC	103
QY	61	CTTTCTCCGAGGCCAGCCAAAGATTATAGCAACACCACTACACTGGTATCAACAAAGGCCT	120
Db	104	CTCTCCTGCAGGGCCAGTCTAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCT	163
QY	121	GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGATCCCCGCC	180
Db	164	GGCCAGGCTCCCAGGCTCCCTCATCTCTGATGCATCCCAACAGGGCCACTGGCATCCCCAGCC	223
QY	181	AGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT	240
Db	224	AGGTTCAAGTGGCAGTGGGCTGGGACAGAGTTCACCTCACCATCAGCAGCCTAGAGCCT	283
QY	241	GAGATTTTCAGTCTATTACTCTCAACAGAGTGGCAGCTGGCCTCACAGTTCGGAGGG	300
Db	284	GAGATTTTCAGTCTATTACTGTACAGCGTAGCAACTGGGCTTGACAGCTTCGGCCAA	343
QY	301	GGGACCAAGTGGAAATTA	320
Db	344	GGGACCAAGTGGGAAGTCAA	363

RESULT	6
AV733856	
LOCUS	482 bp mRNA EST
DEFINITION	AV733856 cda Homo sapiens cDNA clone cdABA01 5', mRNA sequence.
ACCESSION	AV733856
VERSION	AV733856.1 GI:10851401
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;





REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 624)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Invitro Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM8561 row: g column: 20  
High quality sequence stop: 598.

FEATURES  
source

1..624  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J (f129)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3501355"  
/clone\_lib="NCI CGAP Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT  
ORIGIN

172 a 166 c 145 g 141 t  
Query Match 62.8%; Score 201.6; DB 166; Length 624;  
Best Local Similarity 76.9%; Pred. No. 5.5e-52;  
Matches 246; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACAGCTCCAGCCACCCGTCTCTCAGCCCGAGGAGGCGACT 60  
DB 59 GACATCTTGATGACCCAGCTCCAGCCACCCGTCTGTGACTCCAGGAGAACAGTCACT 118  
QY 61 CTTTCTGCGCAGCGCAGCAAGATATTAGCAACCACTACACTGCTATCAACAAGGCGCT 120  
DB 119 CTTTCTGTAGCGCCAGCCAGCAATATTACAAAGAACCTACACTGCTATCAACAGAAATCA 178  
QY 121 GGTCAAGCCCAAGCTCTCATCAAGTATCGTTCCAGTCCATCTCTGGATCCCGCC 180  
DB 179 CATGGACTCCAGGCTCTCATCAAGTATGCACCTGATCCCATCTCTGGATCCCGCTCC 238  
QY 181 AGGTTCACTGGCAGTGGATCAGGACAGATTTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
DB 239 AGGTTCACTGGCAGTGGATCAGGACAGATTTACACTCTCATCACTATCAACAGTGTGAAGCT 298  
QY 241 GAAGATTTGCACTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300  
DB 299 GAAGATGAAGGAATATTACTGTCTTCAAGGTACAGCATGCCGTATACGTTCCGATCG 358  
QY 301 GGGACCAAGTGGAAATATA 320  
DB 359 GGGACCAAGCTGGAAATAA 378

RESULT 9  
AW405025

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW405025 385 bp mRNA EST 16-FEB-2000  
UI-HF-BL0-abx-e-03-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
IMAGE:3058252 5', mRNA sequence.  
AW405025  
AW405025.1 GI:6924082  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 385)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward.

FEATURES  
source

1..385  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3058252"  
/clone\_lib="NIH\_MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: pT73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT  
ORIGIN

88 a 114 c 98 g 85 t  
Query Match 62.7%; Score 201.2; DB 115; Length 385;  
Best Local Similarity 77.0%; Pred. No. 6.3e-52;  
Matches 245; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 3 GATTGTGCTAACTAGTCTCCAGCCACCCGTCTCTCAGCCCGAGGAGGCGACTCT 62  
DB 7 GATTGTGTTGACACAGTCTCCAGCCACCCGTCTTGTCTCCAGGGGAAAGACCCCT 66  
QY 63 TTCTGCCAGGCGAGCAAGTATTAGCAACCACTACACTGTGTATCAACAAGGCGCTGG 122  
DB 67 CTCTGCGAGGCGAGTCAAGTGTTCGAGCTACTTAGCTGTGTACACAGAACTGG 126  
QY 123 TCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGATCCCGCCAG 182  
DB 127 CCAGGCTCCAGGCTCTCATCTATGATCATCAACAGGCGCACTGGCATCCAGCCAG 186  
QY 183 GTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCATCTATCTCCAGTCTGGAGCTGA 242  
DB 187 GTTCAGTGGCAGTGGGCTCTGGGACAGACTTCTCTCACCATCAGCAGCTAGAGCTGA 246  
QY 243 AGATTTTGCACTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGGG 302  
DB 247 AGATTTTGCACTATTACTGTGTCAGCAGCAAGGCACTGGCCCTCGGACGCTTGGCCAGG 306  
QY 303 GACCAAGGTGGAAATATA 320  
DB 307 GACCAAGGTGGAAATCAA 324

RESULT 10  
AW405643

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AW405643 468 bp mRNA EST 16-FEB-2000  
UI-HF-BL0-abs-f-05-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
IMAGE:3057561 5', mRNA sequence.  
AW405643  
AW405643.1 GI:6924700  
EST.  
human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 468)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.

FEATURES  
source  
1..468  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3057561"  
/tissue\_lib="NIH\_MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: pT7f3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
BASE COUNT 110 a 137 c 115 g 106 t  
ORIGIN

Query Match 62.3%; Score 200; DB 115; Length 468;  
Best Local Similarity 76.6%; Pred. No. 1.6e-51;  
Matches 245; Conservative 0; Mismatches 75; Indels 0; Gaps 0;  
QY 1 GAGATTGCTAACTAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 23 GAAATTTGTTGACACAGTCTCCAGCCACCTGCTCTTGTCTCCAGGGGAAAGGCCACC 82  
QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAGGCCT 120  
DB 83 CTCCTCGCAGGCGCAGTACAGGCTTAGCGGCTACTTAGCCTGTACCAACAGACCT 142  
QY 121 GGTCAGCCCCAAGGCTTCATCAAGTATGTTCCAGTCCCATCTCTGGGATCCCCGCC 180  
DB 143 GGCAGGCTCCAGGCTCCCTCATCTATGATGATCCCAACAGGGCCACTGGCATCCAGCC 202  
QY 181 AGGTTTCAGTGCAGTGCAGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCCT 240  
DB 203 AGGTTTCAGTGCAGTGGCTGGGACAGACTTCACTCTACCATCAGCAGCTAGAGCCT 262  
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACAGTTCCGGAGG 300  
DB 263 GAAGATTTCAGTCTATTACTGTGTCAGCGTAGCAACTGGCGGTCACCTTCGGCCCT 322  
QY 301 GGGACCAAGTGGAAATTA 320  
DB 323 GGGACCAAGTGGATCA 342

RESULT 11  
AW04506 468 bp mRNA EST 16-FEB-2000  
LOCUS  
DEFINITION UI-HF-BLO-aby-a-05-01.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
IMAGE:3058065 5', mRNA sequence.  
ACCESSION AW04506  
VERSION AW04506.1 GI:6923563

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 468)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.

FEATURES  
source  
1..468  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3058065"  
/tissue\_lib="NIH\_MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: pT7f3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
BASE COUNT 106 a 137 c 114 g 111 t  
ORIGIN

Query Match 61.8%; Score 198.4; DB 115; Length 468;  
Best Local Similarity 76.2%; Pred. No. 5e-51;  
Matches 244; Conservative 0; Mismatches 76; Indels 0; Gaps 0;  
QY 1 GAGATTGCTAACTAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 41 GAAATTTGTTGACACAGTCTCCAGCCACCTGCTCTTGTCTCCAGGGGAAAGGCCACC 100  
QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAGGCCT 120  
DB 101 CTCCTCGCAGGCGCAGTACAGGCTTAGCGCTACTTAGCCTGGTACCAACAGAAACCT 160  
QY 121 GGTCAGCCCCAAGGCTTCATCAAGTATGATGATCCCAACAGGGCCACTGGCATCCAGCC 180  
DB 161 GGCAGGCTCCAGGCTCCCTCATCTATGATGATCCCAACAGGGCCACTGGCATCCAGCC 220  
QY 181 AGGTTTCAGTGCAGTGCAGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCCT 240  
DB 221 AGGTTTCAGTGCAGTGGCTGGGACAGACTTCACTCTCACCATCAGCAGCTAGAGCCT 280  
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGTTCCGGAGG 300  
DB 281 GAAGATTTCAGTCTATTACTGTGTCAGCAGCGTAGCAACTGGTGTACAGCTTTTGGCCAG 340  
QY 301 GGGACCAAGTGGAAATTA 320  
DB 341 GGGACCAAGTGGAGATCA 360

RESULT 12  
BG536848 1015 bp mRNA EST 03-APR-2001  
LOCUS  
DEFINITION BG536848 1015 bp mRNA EST 03-APR-2001  
IMAGE:602566386F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4691085 5',  
mRNA sequence.



[illegible]

Search completed: October 11, 2001, 14:34:02  
Job time: 5539 sec

---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:35 ; Search time 177.65 seconds  
(without alignments)  
1134.570 Million cell updates/sec

Title: US-08-791-391A-3  
Perfect score: 321  
Sequence: 1 GAGATTGTGCTACTCAGTC.....GGACCAAGGTGGAATTAAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues 1460202  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*  
1: /SIDSI/gcgdata/geneseq/geneseq/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	19 AAV49821	Vitaxin antibody 1
2	321	100.0	321	22 AAF28176	Vitaxin light chain
3	318.6	99.3	321	19 AAV49843	LM609 antibody lig
4	318	99.1	321	22 AAF28199	DNA encoding light
5	268.2	83.6	321	19 AAV49823	LM609 antibody lig
6	268.2	83.6	321	22 AAF28178	Antibody LM609 lig
7	260.8	81.2	381	21 AA235244	Humanised anti-ver
8	252.8	78.8	321	20 AAV71800	Humanised anti-alp
9	252.8	78.8	338	20 AAV71802	Vitronectin alpha
10	248	77.3	381	15 AAQ64167	Sequence of mouse
11	248	77.3	381	22 AAF58747	Murine CMV5 antibo

12	241.6	75.3	324	20	AAV71798	Murine vitronectin
13	241.6	75.3	5238	11	AAQ04654	Plasmid pBT111 enc
14	235.2	73.3	381	21	AAZ35242	Mouse anti-verotox
15	233.6	72.8	651	21	AAA44346	Human secreted exp
16	232	72.3	416	18	AAAT49345	cDNA encoding kapp
17	230.4	71.8	324	17	AAAT33446	EGF receptor chime
18	230.4	71.8	415	21	AAAD0904	Humanised antibody
19	230.4	71.8	415	21	AAAD0906	Humanised antibody
20	225.6	70.3	8858	20	AAZ10202	Expression vector
21	224	69.8	363	17	AAAT38510	Light chain coding
22	224	69.8	486	14	AAQ43245	hIL2R Ab L chain v
23	220.8	68.8	415	21	AAAD01262	Mouse monoclonal a
24	219	68.2	315	20	AAV71803	Jk gene segment.
25	219	68.2	315	20	AAV71805	Humanised anti-alp
26	216	67.3	322	15	AAQ44714	Light chain variab
27	216	67.3	322	15	AAZ28545	Light chain variab
28	214.4	66.8	321	20	AAZ10203	DNA encoding the v
29	209.6	65.3	321	20	AAZ10205	DNA encoding the v
30	208	64.8	322	14	AAQ36615	Anti-IL2R-beta ant
31	208	64.8	1395	10	AAAN90300	Insert coding for
32	206.4	64.3	321	14	AAQ43243	B-B10 Mab L chain
33	206.4	64.3	321	19	AAV26766	Anti-gp54 Mab 48-1
34	206.4	64.3	324	22	AAAF29505	Human Fab clone LD
35	206.4	64.3	486	14	AAQ43384	L-chain V-region o
36	204.8	63.8	321	21	AAA40203	H. pylori beta-ure
37	204.8	63.8	381	18	AAAT49338	cDNA encoding kapp
38	204.8	63.8	416	18	AAAT49344	cDNA encoding kapp
39	204.8	63.8	416	18	AAAT49342	cDNA encoding kapp
40	203.4	63.4	318	14	AAQ48766	Monoclonal antibod
41	203.2	63.3	381	19	AAV12262	Monoclonal antibod
42	203.2	63.3	642	20	AAV77408	Anti-human TNF-alp
43	202.2	63.0	720	19	AAAT26770	Anti-gp54 Mab 48-1
44	201.6	62.8	794	17	AAAT42033	Plasmid pMW152-225
45	201.6	62.8	2070	17	AAAT42035	Plasmid pSW202-225

## ALIGNMENTS

RESULT 1	
AAV49821	
ID	AAV49821 standard; DNA; 321 BP.
AC	AAV49821;
XX	
XX	
DT	02-NOV-1998 (first entry)
XX	
DE	Vitaxin antibody light chain variable region DNA.
XX	
KW	Vitaxin; antibody; variable region; heavy chain; integrin;
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW	macular degeneration; osteoporosis; ss.
XX	
OS	Mus sp.
XX	
FH	key
FT	CDS
FT	Location/Qualifiers
FT	1..321
FT	/*tag= a
FT	/product= "vitaxin antibody light chain variable region"
FT	/note= "partial sequence, no start or stop codon given"
XX	
PN	WO9833919-A2.
XX	
PD	06-AUG-1998.
XX	
PF	30-JAN-1998; 98WO-US01826.
XX	
PR	30-JAN-1997; 97US-0791391.
XX	
PA	(IXSY-) IXSYS INC.
XX	







Db 121 ggtaagcccaaggcttctcatennntatctgttccagtcctatctctgtggatccccgcc 180  
QY 181 AGGTTCAAGTGGCAGTGCAGGACAGATTTCACCTCCTCACTATCTCCAGTCTGGAGCCT 240  
Db 181 aggttcagtgccagtgatcaggagacagattccaccctcactatctccagctcggagcct 240  
QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGGAGGG 300  
Db 241 gaagatttgcagtcattactgtcaacagagtggcagctggcctcacacagtttcggagg 300  
QY 301 GGGACCAAGTGGAAATTAAG 321  
Db 301 gggaccaagtggaattaag 321

## RESULT 5

AAV49823  
ID AAV49823 standard; DNA; 321 BP.  
XX  
AC AAV49823;  
XX  
DT 02-NOV-1998 (first entry)  
XX  
DE LM609 antibody light chain variable region DNA fragment.  
XX  
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; ss.  
XX  
OS Mus sp.

## Mus sp.

XX  
FH Key Location/Qualifiers  
FT CDS 1..321  
FT /tag= a  
FT /product= "LM609 antibody light chain variable region"  
FT /note= "partial sequence, no start or stop codon given"  
XX  
PN WO9833919-A2.  
XX  
PD 06-AUG-1998.  
XX  
PF 30-JAN-1998; 98WO-US01826.  
XX  
PR 30-JAN-1997; 97US-0791391.  
XX  
PA (IXSY-) IXSYS INC.  
XX  
PI Glaser SM, Huse WD;  
XX  
WPI; 1998-437472/37.  
DR P-PSDB; AAW75004.  
XX  
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX

## Claim 40; Fig 2b; 129pp; English.

XX  
CC This sequence encodes the LM609 antibody variable light chain region.  
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
CC block integrin-mediated signal transduction. This is useful in the  
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
CC etc.). The antibodies contain non-murine framework regions so are  
CC suitable for use in humans. Enhanced types of LM609 have affinity more  
CC than 90 times greater than that of parent the parent antibody.

SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;  
Query Match 83.6%; Score: 268.2; DB 19; Length 321;  
Best Local Similarity 89.7%; Pred. No. 4.8e-75;  
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTCTCTCTCAGCCAGGAGAAAGGGGACT 60  
Db 1 gatattgtctaaactcagtcctccagccaccctgtctgtcacaccaggagatagcgtcagt 60  
QY 61 CTTTCTCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACTACTGGTATCAACAAGGCCT 120  
Db 61 ctttctctgccaggccagccaaagtattagcaaccacactacactggtatcaacaaaaatca 120  
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCTTCCAGTCTCTGGATCCCCGCC 180  
Db 121 catgagctctccaggcttctcatcaagtatcgttccagtcctatctctggatccccctcc 180  
QY 181 AGGTTCAAGTGGCAGTGCAGGACAGATTTCACCTCCTCACTATCTCCAGTCTGGAGCCT 240  
Db 181 aggttcagtgccagtgatcaggagacagatttctcagtcctcagtatcaacagtgaggact 240  
QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGGAGGG 300  
Db 241 gaagatttggaaatgtatttctgtcaacagagtggcagctggcctcacacggttcggagg 300  
QY 301 GGGACCAAGTGGAAATTAAG 321  
Db 301 gggaccaagctggaaattaag 321

## RESULT 6

AAF28178  
ID AAF28178 standard; DNA; 321 BP.  
XX  
AC AAF28178;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Antibody LM609 light chain variable region DNA.  
XX  
KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
XX  
DR WPI; 2001-050110/06.  
XX  
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX  
PS Disclosure; Fig 2; 132pp; English.  
XX  
CC The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphavbeta3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 83.6%; Score 268.2; DB 22; Length 321;  
 Best Local Similarity 89.7%; Pred. No. 4.8e-75;  
 Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
 Qy 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAGGCGACT 60  
 Db 1 gatattgtctaactcagctctccagccaccctgtctgtgacacccaggagatagcgtcagt 60  
 Qy 61 CTTTCTCCAGCCAGGCAAGTATTAGCAACACCTACACTGCTGATCAACAAGGCGCT 120  
 Db 61 ctttctccagggcagccaaagtattagcaaccactacactggtatcaacaaaatca 120  
 Qy 121 GGTCAAGCCCAAGCTTCTCATCAAGTATCGTTCCTCAGTCACTCTCGGATCCCGCC 180  
 Db 121 catgagttccaaaggcttctcatcaagtatcgttccagtcctatctctggatccctcc 180  
 Qy 181 AGTTTCAGTGGCAGTGATCAGGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
 Db 181 agtttcagtgccagtgagatcaggacagatttcgctctcagtatcaacagtgtggagact 240  
 Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGGG 300  
 Db 241 gaagattttggaagtattctgtctcaacagatggcagctggcctcacacgttcggagg 300  
 Qy 301 GGGACCAAGTGGAAATTAAG 321  
 Db 301 gggaccaagctggaaattaag 321

RESULT 7  
 AAZ35244  
 ID AAZ35244 standard; cdna; 381 BP.  
 XX  
 AC AAZ35244;  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Humanised anti-verotoxin II antibody Vtm1-1 VL cdna.  
 XX  
 KW Verotoxin II; VT2; shiga-like toxin; Vtm1-1; MuVtm1-1;  
 KW monoclonal antibody; light chain; mouse; human; humanised antibody;  
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
 KW HUS; therapy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT /\*tag= a  
 FT mat\_peptide 61..381  
 FT /\*tag= b  
 XX  
 PN W09959629-A1.  
 XX  
 XX 25-NOV-1999.  
 PD  
 PF 19-MAY-1999; 99WO-US11179.  
 XX  
 XX 20-MAY-1998; 98US-0086570.  
 PR  
 XX (TEIJ ) TEIJIN LTD.  
 PA (PROT-) PROTEIN DESIGN LABS INC.

XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;  
 PI WPI; 2000-086580/07.  
 DR P-PSDB; AAY32407.  
 DR  
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli -  
 PT  
 XX Disclosure; Fig 2b; 59pp; English.  
 XX  
 CC This DNA sequence codes for a humanised light chain variable region  
 CC (see AAY32407) of murine monoclonal antibody Vtm1-1 (MuVtm1-1), an  
 CC antibody that specifically binds to the B subunit of verotoxin II  
 CC (VT2). The invention relates to humanised antibodies against VT2  
 CC that are capable of neutralizing VT2 and/or VT2 variants. The  
 CC humanised antibody is a humanized form of MuVtm1-1 comprising the  
 CC complementarity determining regions of MuVtm1-1 (see AAY32404-05) and  
 CC heavy and light chain variable region frameworks from the human GF4  
 CC antibody heavy and light chain frameworks, provided that at least 1  
 CC position selected from L49, H29, H30, H49 and H98 is occupied by the  
 CC amino acid at the equivalent position of the MuVtm1-1 antibody heavy  
 CC or light chain variable region framework. Such humanized antibodies  
 CC have an affinity for VT2 that is 3-, 5 or 10-times that of MuVtm1-1.  
 CC They are used for treating a patient suffering from, or at risk of,  
 CC the toxic effects from VT2 (claimed), especially for treating  
 CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic  
 CC uraemic syndrome (HUS).  
 XX  
 SQ Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;

Query Match 81.2%; Score 260.8; DB 21; Length 381;  
 Best Local Similarity 88.4%; Pred. No. 1.1e-72;  
 Matches 283; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
 Qy 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAGGCGACT 60  
 Db 61 gaaattgtctaactcagctctccagccaccctgtctgtctccaggaagaagagccact 120  
 Qy 61 CTTTCTCCAGCCAGGCAAGTATTAGCAACACCTACACTGCTGATCAACAAGGCGCT 120  
 Db 121 cttctctcagggccagtcacaaactattagcaaacactacactggtatcaacaaaacca 180  
 Qy 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCTCAGTCCATCTCTGGGATCCCGCC 180  
 Db 181 ggtcaggccccaaggcttctcatcaagctctctccagtcctcatctctggtatcccccgc 240  
 Qy 181 AGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
 Db 241 aggttcagtgccagtggtatcagggacagatttctcactctcactatcagcagctggaatct 300  
 Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGGG 300  
 Db 301 gaagattttgcagtgattactgtcaacagagattacagctggtcgcagctcagctcggtca 360  
 Qy 301 GGGACCAAGTGGAAATTA 320  
 Db 361 gggaccaagggtggagatcaaa 380  
 RESULT 8  
 AA71800  
 ID AA71800 standard; cdna; 321 BP.  
 XX  
 AC AA71800;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Humanised anti-alpha-v beta-3 Mab D12H2HC 1-0 VL cdna.  
 XX  
 KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;



Db 1 gacatagtagtactgactcagctccaggcaccctgtcttcttcctccaggagaaagagccacc 60  
Qy 61 CTTTCTCCAGCGCCAGCAAGTATTAGCAACCACTACACTGCTATCAACAAGGCT 120  
Db 61 cttctctcaggcgccagcgaagattagcaaccctacactggtatcaacaacaact 120  
Qy 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGGC 180  
Db 121 ggcaggctcgcggcttctcatcaagtagcttcccaagtcattctgggaccctcc 180  
Qy 181 AGTTTCAGTGGCAGTGGATGAGGACAGATTCACCTCACATCTCCAGTCTGGAGCT 240  
Db 181 aggttcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240  
Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTCCGAGG 300  
Db 241 gaagattttgcggttattactgtcaacagagtaaacagctggccttccacgttcgagcag 300  
Qy 301 GGGACCAAGGTGGAATTA 320  
Db 301 ggtaccaaggtggaataaa 320

RESULT 10  
AAQ64167  
ID AAQ64167 standard; cDNA to mRNA; 381 BP.  
AC AAQ64167;  
XX  
DT 29-DEC-1994 (first entry)

XX Sequence of mouse V-kappa showing the sequences of recombinant  
DE anti-FHV-1 antibody CDRs 1, 2 and 3.  
XX Feline herpes virus; FHV-1; monoclonal antibody; CDR;  
KW complementarity determining region; ss.  
XX Mus musculus.

Key Location/Qualifiers  
FT CDS 1..381  
FT /\*tag= a  
FT misc\_feature 19  
FT /\*tag= b  
FT /\*label= MKL104  
FT misc\_feature 385..429  
FT /\*tag= C  
FT /\*label= MKL124

XX WO9412661-A.  
XX 09-JUN-1994.  
XX 25-NOV-1993; 93WO-JP01724.  
XX 28-NOV-1992; 92JP-0341255.  
XX (KAGA ) CEMO SERO THERAPEUTIC RES INST.  
XX Kinachi K, Maeda H, Nishiyama K, Tokiyoshi S;  
XX WPI; 1994-200288/24.  
XX P-PSDB; AAR54093.

XX Feline monoclonal antibody and recombinant antibodies specific  
PT for FHV-1 - for detection, treatment and prevention of FHV-1  
PT infection.  
XX Disclosure; Page 18-19; 53pp; Japanese.  
XX The inventors claim a monoclonal antibody against feline herpes  
CC virus (FHV-1). They also claim a recombinant antibody against FHV-1

CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are  
CC used in the detection, treatment and prevention of FHV-1. The  
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1  
CC antibody are given in AAR54092. The sequences of the CDRs in the VL of  
CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR  
CC sequences are claimed.  
XX  
SQ Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;

Query Match 77.3%; Score 248; DB 15; Length 381;  
Best Local Similarity 85.9%; Pred. NO. 1.2e-68;  
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
Qy 1 GAGATTGTCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60  
Db 61 gatatgtgctaaactcagctccagccacctgtctgtgactccaggagatagcagct 120  
Qy 61 CTTTCTCCAGCGCCAGCAAGTATTAGCAACCACTACACTGCTATCAACAAGGCT 120  
Db 121 cttctctcaggcgccagcgaagattagcaaccctacactggtatcaacaacaact 180  
Qy 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCGGC 180  
Db 181 catgagttctcaaggcttctcatcaagtagcttcccaagtcattctgggaccctcc 240  
Qy 181 AGTTTCAGTGGCAGTGGATGAGGACAGATTCACCTCACATCTCCAGTCTGGAGCT 240  
Db 241 aggttcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300  
Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTCCGAGG 300  
Db 301 gaagattttgcggttattactgtcaacagagtaaacagctggccttccacgttcgagcag 360  
Qy 301 GGGACCAAGGTGGAATTA 320  
Db 361 gggaccaaggtgagctgaa 380

RESULT 11  
AAF58747  
ID AAF58747 standard; cDNA; 381 BP.  
XX  
AC AAF58747;  
XX  
DT 30-APR-2001 (first entry)  
XX Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.  
DE Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;  
KW light chain; graft versus host disease; transplant; autoimmune disease;  
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;  
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;  
KW ss.  
XX Mus sp.  
OS  
XX US6180370-B1.  
PN  
XX 30-JAN-2001.  
PD  
XX 07-JUN-1995; 95US-0484537.  
PF  
XX 28-DEC-1988; 88US-0290975.  
PR  
XX 13-FEB-1989; 89US-0310252.  
PR  
XX 28-SEP-1990; 90US-0590274.  
PR  
XX 19-DEC-1990; 90US-0634278.  
XX  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
XX Queen CL, Selick HE;  
PI  
XX WPI; 2001-190856/19.  
DR

DR P-PSDB; AAB69687.  
 XX  
 CC Producing humanized immunoglobulin, involves producing a cell  
 PT containing DNA segments encoding humanized heavy and light chain  
 PT variable regions, and expressing the DNA segments in the cell -  
 XX  
 XX Example 8; Fig 39; 145pp; English.  
 PS  
 XX The present invention describes a method of producing humanised  
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a  
 CC humanised version of an immunoglobulin. This is obtained by comparing a  
 CC donor and human immunoglobulin and producing a combined antibody which  
 CC contains part of each. These are useful in the treatment of  
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such  
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis  
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections  
 CC and myeloid leukaemia. The present sequence is an antibody cDNA used to  
 CC demonstrate the method of the invention.  
 XX  
 XX Sequence 381 BP; 97 A; 92 C; 89 G; 103 T; 0 other;  
 SQ  
 Query Match 77.3%; Score 248; DB 22; Length 381;  
 Best Local Similarity 85.9%; Pred. No. 1.2e-68;  
 Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
 QY 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 GATATTGTCTAACTCAGTCTCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGACT 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 ctttcctgcaggccagccaaagtattagcaacaactacactggtatcaacaataca 180  
 QY 121 GGTCAAGCCCAAGGCTTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCGCC 180  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 catgagtctccaggctctcatcaagtatgcttccagtcctcatctctggatccctcc 240  
 QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCTACTATCTCCAGTCGGAGCCT 240  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 aggttcagtgccagtgagcagagacagattcactctcagtgatcaacggtgaggact 300  
 QY 241 GAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 gaagattttggaatgtattctgtcaacagagtaacagttggcctcatacgttcgagg 360  
 QY 301 GGGACCAAGGTGGAATTA 320  
 Db ||||||||||||||||||||  
 Db 361 gggaccaagctggaaataaa 380  
 RESULT 12  
 AAV71798  
 ID AAV71798 standard; cDNA; 324 BP.  
 XX  
 AC AAV71798;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Murine vitronectin alpha-v beta-3 receptor MAB VL cDNA.  
 XX  
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.  
 XX  
 XX Mus sp.  
 OS  
 XX WO9840488-A1.  
 PN  
 XX 17-SEP-1998.  
 PD

XX 12-MAR-1998; 98WO-US04987.  
 XX  
 XX 12-MAR-1997; 97US-0039609.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA  
 XX  
 XX Johanson KO, Jonak ZL, Taylor AH;  
 PI  
 XX  
 XX WPI: 1999-034590/03.  
 DR  
 DR P-PSDB; AAW84094.  
 XX  
 PT New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis  
 XX  
 PS Example 13; Page 59-60; 97pp; English.  
 XX  
 CC This cDNA sequence codes for the light chain variable region (VL,  
 CC see AAW84094) of the anti-human alpha-v beta-3 vitronectin receptor  
 CC murine monoclonal antibody D12. It was obtained from hybridoma  
 CC total RNA by RT-PCR using mouse kappa and N-terminal-based primers  
 CC (see AAV71808-09). A heavy chain variable region clone (see AAV71797)  
 CC has also been identified. D12 VH and VL show sequence similarity  
 CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see  
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see  
 CC AAW84098) were constructed by combining the framework regions of the  
 CC human V region consensus sequences with complementarity determining  
 CC regions of D12 (keeping some preferred murine framework residues).  
 CC The humanised antibodies are specifically reactive with the human  
 CC alpha-v beta-3 protein receptor and capable of neutralising the  
 CC receptor. They can be used for passive immunotherapy of a disorder  
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular  
 CC disorders or angiogenic-related disorders, such as angiogenesis  
 CC associated with diabetic retinopathy, atherosclerosis and  
 CC restenosis, chronic inflammatory disorders, macular degeneration,  
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and  
 CC diseases where bone resorption is associated with pathology such as  
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia  
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone  
 CC loss due to immobilisation or sex hormone deficiency. They can also  
 CC be used for targeted drug therapy, and for detection and diagnosis.  
 XX  
 SQ Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;  
 Query Match 75.3%; Score 241.6; DB 20; Length 324;  
 Best Local Similarity 84.7%; Pred. No. 1.1e-66;  
 Matches 271; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
 QY 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 gacattgtgtcactcagtcctccagccaccctgtctgtgactccagagatagcgtcagt 60  
 QY 61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 ctttcctgcaggccagccaaagtattagcaaccactacactggtatcaacaagatca 120  
 QY 121 GGTCAAGCCCAAGGCTTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCGCC 180  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 catgagtctccaggctctcatcaagtatgcttccagtcctcatctctggatccctcc 180  
 QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCTACTCTCCAGTCGGAGCCT 240  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 aggttcagtgccagtgatcagcagagacagatttcaactctcaataatcaattttggagact 240  
 QY 241 GAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 gaggattttggaatgtattctgtcaacagagtaacagctggccttcactcgttcgctcg 300  
 QY 301 GGGACCAAGGTGGAATTA 320  
 Db ||||||||| ||||||||| ||

```
Db 301 gggacaaactggaaataaa 320
RESULT 13
AAQ04654
ID AAQ04654 standard; DNA; 5238 BP.
XX
AC AAQ04654;
XX
DT 01-OCT-1990 (first entry)
XX
DE Plasmid pBT111 encoding antibody MAK33 kappa chain.
XX
KW Antibody MAK33; kappa chain; plasmid pBT111; activated antibody; ss.
XX
XX
XX Key Location/Qualifiers
XX CDS 7..663
XX FT /*tag= a
XX FT /product= kappa chain of MAK33
XX
XX DE3835350-A.
XX
XX 19-MAR-1990.
XX
XX 17-OCT-1988; 88DE-3835350.
XX
XX 17-OCT-1988; 88DE-3835350.
XX
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
XX Rudolph R, Buchner J, Lenz H;
XX
XX WPI; 1990-156813/21.
XX
XX Activated antibody prodn. from recombinant procaryotic cells -
XX by solubilisation under reducing conditions, then oxidative
XX renaturation, carried out at low protein concn.
XX
XX Disclosure; ; p; German.
XX
XX Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding
XX the Fd chain of antibody MAK33 were used to transform E.coli DSM 3689
XX and the resulting cells grown to form inclusion bodies. After the final
XX renaturation step an 18% yield of biologically-active protein was
XX produced.
XX see also AAQ04655.
XX
XX Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;
SQ
```

```
Query Match 75.3%; Score 241.6; DB 11; Length 5238;
Best Local Similarity 84.7%; Pred. No. 3e-66;
Matches 271; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTAGTCTCCAGCACCCCTGTCCTCAGCCGAGGAAAGGGCGACT 60
  |||||
Db 7 gatattgtctaactcagtcctccagccaccctgtctgtactccaagatagcgtcagt 66

QY 61 CTTTCTCCAGGCGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCCT 120
  |||||
Db 67 cttctcgcagggccagcagaagtattagcaacaacctacactggtatcaacaagaatca 126

QY 121 GGTCAGCCCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
  |||||
Db 127 catgagtcctcaaggctctcatcaaatagctcccgagtcctctctggtatccctct 186

QY 181 AGGTTAGTGGCAGTGGTACAGGACAGATTTCACCTCTCACTATCTCCAGTCTCGAGCCT 240
  |||||
Db 187 aggttcagtgccagtgatcaggagacagatttcaactctcagtatcaaacagtgtagact 246

QY 241 GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCGAGCTGGCCTCAACAGTTTCGGAGGG 300
  |||||
Db 247 gaagattttggaatgtattctctgtcaacagagtaaacagctggcctctcaagtcggtgct 306
```

```
QY 301 GGACCAAGGTGGAATTAA 320
  |||||
Db 307 gggaccaagctggagctgaa 326

RESULT 14
AAZ35242
ID AAZ35242 standard; CDNA; 381 BP.
XX
AC AAZ35242;
XX
XX 13-MAR-2000 (first entry)
XX
XX Mouse anti-verotoxin II antibody VTml-1 VL CDNA.
XX
XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
XX monoclonal antibody; light chain; mouse; humanised antibody;
XX Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
XX HUS; therapy; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX FT sig_peptide 1..60
XX FT /*tag= a
XX FT mat_peptide 58..381
XX FT /*tag= b
XX FT /transl_except= (pos:184..186, aa:Lys)
XX
XX WO9959629-A1.
XX
XX 25-NOV-1999.
XX
XX 19-MAY-1999; 99WO-US11179.
XX
XX 20-MAY-1998; 98US-0086570.
XX
XX (TEIJ ) TEIJIN LTD.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX
XX WPI; 2000-086580/07.
XX P-PSDB; AAY32405.
XX
XX Humanized antibody binding to verotoxin II used for treating Verotoxin
XX producing E. coli -
XX
XX Disclosure; Fig 1b; 59pp; English.
XX
XX This DNA sequence codes for the light chain variable region (see
XX AAY32405) of murine monoclonal antibody Vtml-1 (MuVTml-1), an
XX antibody that specifically binds to the B subunit of verotoxin II
XX (VT2). The invention relates to humanised antibodies against VT2
XX that are capable of neutralizing VT2 and/or VT2 variants. The
XX humanized antibody is a humanized form of MuVTml-1 comprising the
XX complementarity determining regions of MuVTml-1 and heavy and
XX light chain variable region frameworks from the human GF4 antibody
XX heavy and light chain frameworks, provided that at least 1 position
XX selected from L49, H29, H30, H49 and H98 is occupied by the amino
XX acid at the equivalent position of the MuVTml-1 antibody heavy or
XX light chain variable region framework. Such humanized antibodies
XX (see AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times
XX that of MuVTml-1. They are used for treating a patient suffering
XX from, or at risk of, the toxic effects from VT2 (claimed), especially
XX for treating verotoxin producing Escherichia coli (VTEC) infection,
XX and haemolytic uraemic syndrome (HUS).
XX
XX Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;
SQ
```

Query Match 73.3%; Score 235.2; DB 21; Length 381;

Best Local Similarity 83.4%; Pred. No. 1.2e-64; Matches 267; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGCCAGCCCTCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 61 gatgtgtgtaactcagctccagccacctgtctgtgactccagagatagcgtcagt 120  
QY 61 CTTTCTCTCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120  
DB 121 ctttctcagggccagtcgaactattagcaaacactacactggtatcaacacaaatca 180  
QY 121 GGTCAAGCCCCAAGGCTCTCTCAATCAAGTATCGTTCACGATCCATCTCTGGATCCCGCC 180  
DB 181 catgagctcccaaggcttctcatcaagtctgtctccagtcctatctctggtatccctcc 240  
QY 181 AGGTCAGTGGCAGTGATTCAGGACAGATTTACCCCTCACTATCTCCAGTGGAGCCT 240  
DB 241 aggttcagtgccagtggtgacggagcagattcctcctcagtcacacagtggtgaaact 300  
QY 241 GAAGATTTGCGAGTCTTATCTCACTCAAGTATCGTTCACGATCCATCTCTGGATCCCGCC 300  
DB 301 gaagatttggaatgatttctgtcaacagagttacagctgcccgtcagcttcggtgct 360  
QY 301 GGGACCAAGTGGAAATTTAA 320  
DB 361 gggaccaagctggagctgaa 380

RESULT 15

AAAA4346

ID AAA44346 standard; cDNA; 651 BP.

XX AC AAA44346;

XX DT 21-AUG-2000 (first entry)

XX DE Human secreted expressed sequence tag SEQ ID NO:921.

XX KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;  
KW expressed sequence tag; EST; probe; chemotactic; proliferative;  
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;  
KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;  
KW antiviral; antidiabetic; antisthmatic; vulnerary; antiparkinsonian;  
KW antitumor; osteopathic; neuroprotective; nootropic; antipsoriatic;  
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;  
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;  
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;  
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
KW central nervous system disorder; Alzheimer's disease; stroke;  
KW Parkinson's disease; Huntington's disease; coagulation disorder;  
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;  
KW tumour; infection; depression; psoriasis; ss.

XX OS Homo sapiens.

XX PN WO200021991-A1.

XX PD 20-APR-2000.

XX PF 15-OCT-1999; 99WO-US24206.

XX PR 15-OCT-1998; 98US-0104436.

XX PA (GENY ) GENETICS INST INC.

XX PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;

XX PI Merberg D, Treacy M, Bowman MR;

XX WPI: 2000-317938/27.

XX Isolated polynucleotides, and encoded proteins, comprising secreted  
PT expressed sequence tags (sESTs), useful for treating various disorders  
PT such as autoimmune, infectious, and central nervous system disorders -

XX PS Claim 1; Page 440; 803pp; English.  
XX CC AAA43426 to AAA5925 represent specifically claimed secreted expressed  
CC sequence tags (sESTs), isolated from human, mouse, chicken and rat  
CC tissue sources. The sESTs can have a range of activities depending on  
CC the tissues they were isolated from. The activities include:  
CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;  
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;  
CC antisthmatic; vulnerary; antitumor; osteopathic; neuroprotective;  
CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;  
CC anticonvulsant; and antidepressant. The sESTs can be used for gene  
CC therapy and in vaccines. The sESTs are useful as probes for the  
CC identification and isolation of full-length cDNAs and genomic DNA  
CC molecules which correspond to the sESTs. Proteins encoded by the sESTs  
CC are useful in assays for determining biological activity and raising  
CC antibodies. They may be useful for treatment of autoimmune disorders  
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
CC osteoporosis, osteoarthritis, central nervous system disorders  
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's  
CC disease), tumours, bacterial, fungal or viral infections, depression and  
CC psoriasis. AAA5926 to AAA5931 represent linker variants which are given  
CC in the exemplification of the present invention.  
XX SQ Sequence 651 BP; 174 A; 166 C; 151 G; 160 T; 0 other;

Query Match 72.8%; Score 233.6; DB 21; Length 651;  
Best Local Similarity 83.1%; Pred. No. 4.8e-64;  
Matches 266; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGCCAGCCCTCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 94 gacattgtgactcagctccagccacctgtctgtgactccagagatagctctct 153  
QY 61 CTTTCTCTCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120  
DB 154 ctttctcagggccagccagagattagcagactactacactggtatcaacacaaatca 213  
QY 121 GGTCAAGCCCCAAGGCTCTCTCAATCAAGTATCGTTCACGATCCATCTCTGGATCCCGCC 180  
DB 214 catgagctcccaaggcttctcatcaaatgcttcccaatccatctctggtatccctcc 273  
QY 181 AGGTTTCAGTGGCAGTGATTCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240  
DB 274 aggttcagtgccagtggtgacggggtcagattcctcctcagtcacacagtggtgaaact 333  
QY 241 GAAGATTTGCGAGTCTTATCTCAAGTATCGTTCACGATCCATCTCTGGATCCCGCC 300  
DB 334 gaagatttggaatgatttctgtcaacagagttacagctgcccgtcagcttcggtgagg 393  
QY 301 GGGACCAAGTGGAAATTTAA 320  
DB 394 gggaccaagctggaaataaa 413

Search completed: October 11, 2001, 15:12:36  
Job time: 6468 sec





**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:14:12 ; Search time 87.94 seconds  
(without alignments)  
691.027 Million cell updates/sec

Title: US-08-791-391A-3  
Perfect score: 321  
Sequence: 1 GAGATTGTCTACTAGTC.....GGACCAAGCTGGAATAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	77.3	381	1	US-07-634-278-82
2	248	77.3	381	1	US-08-477-728-82
3	248	77.3	381	1	US-08-474-040-82
4	248	77.3	381	1	US-08-487-200-82
5	248	77.3	381	4	US-08-484-537-82
6	248	77.3	424	1	US-08-436-463-3
7	241.6	75.3	5238	6	5453363-1
8	227.2	70.8	321	2	US-08-232-081B-35
9	224	69.8	321	2	US-08-232-081B-36
10	224	69.8	324	2	US-08-737-560A-13
11	224	69.8	363	2	US-08-737-560A-8
12	216	67.3	322	2	US-08-476-176B-3
13	216	67.3	322	3	US-08-127-721A-3
14	216	67.3	322	3	US-08-485-246A-3
15	206.4	64.3	321	2	US-08-232-081B-39
16	203.4	63.4	318	1	US-08-326-362-3
17	201.2	62.7	318	2	US-08-800-198-3
18	201.2	62.7	318	3	US-09-296-595-3
19	201.2	62.7	720	2	US-08-800-198-7
20	201.2	62.7	720	3	US-09-296-595-7
21	200	62.3	720	2	US-07-956-399-1
22	196.2	61.1	429	2	US-08-653-402B-7
23	193.6	60.3	321	1	US-08-192-102-2
24	193.6	60.3	321	1	US-08-324-799-2
25	193.6	60.3	321	2	US-08-192-861A-2
26	193.6	60.3	717	2	US-07-956-399-3
27	187.6	58.4	812	1	US-08-053-131-178

28	187.6	58.4	812	1	US-08-096-762-178
29	187.6	58.4	812	4	US-09-042-353-41
30	181.2	56.4	900	1	US-08-053-131-180
31	181.2	56.4	900	1	US-08-096-762-180
32	181.2	56.4	900	4	US-09-042-353-43
33	180.8	56.3	931	3	US-09-049-672A-19
34	174.8	54.5	321	4	US-09-240-274-201
35	174.4	54.3	424	2	US-08-476-176B-9
36	174.4	54.3	424	3	US-08-127-721A-9
37	174.4	54.3	424	3	US-08-485-246A-9
38	174.2	54.3	325	5	PCT-US93-12501-1
39	174	54.2	642	2	US-08-480-753-5
40	174	54.2	642	3	US-09-041-889-10
41	174	54.2	642	3	US-08-837-058-10
42	172.8	53.8	424	2	US-08-476-176B-7
43	172.8	53.8	424	3	US-08-127-721A-7
44	172.8	53.8	424	3	US-08-485-246A-7
45	172.2	53.6	321	4	US-09-240-274-216

ALIGNMENTS

RESULT 1  
US-07-634-278-82  
; Sequence 82, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-07-634-278-82

Query Match          77.3%; Score 248; DB 1; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
   |||||||
Db 61 GATATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 120
   |||||||

QY 61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCCT 120
   |||||||
Db 121 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCCT 180
   |||||||

QY 121 GGTCAAGCCCGCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCGCC 180
   |||||||
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCGCC 240
   |||||||

QY 181 AGGTCAGTGGCAGTGGATCCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
   |||||||
Db 241 AGGTCAGTGGCAGTGGATCCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 300
   |||||||

QY 241 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 300
   |||||||
Db 301 GAAGATTGTGGAATGATTTCTGTCAACAGAGTAAAGTGGCCCTCATACGTTTCGGAGGG 360
   |||||||

QY 301 GGGACCAAGGTGGAAATTA 320
   |||||||
Db 361 GGGACCAAGCTGGAATATA 380
   |||||||

RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-477-728-82

Query Match          77.3%; Score 248; DB 1; Length 381;
Best Local Similarity 85.9%; Pred. No. 2.9e-70;
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
   |||||||
Db 61 GATATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 120
   |||||||

QY 61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCCT 120
   |||||||
Db 121 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAAGGCCT 180
   |||||||

QY 121 GGTCAAGCCCGCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCGCC 180
   |||||||
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCGCC 240
   |||||||

QY 181 AGGTCAGTGGCAGTGGATCCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
   |||||||
Db 241 AGGTCAGTGGCAGTGGATCCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 300
   |||||||

QY 241 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 300
   |||||||
Db 301 GAAGATTGTGGAATGATTTCTGTCAACAGAGTAAAGTGGCCCTCATACGTTTCGGAGGG 360
   |||||||

QY 301 GGGACCAAGGTGGAAATTA 320
   |||||||
Db 361 GGGACCAAGCTGGAATATA 380
   |||||||

RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```



Db 241 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300  
QY 241 GAAGATTTTGGCAGTCTATTACTCTCAACAGAGTGGCAGTGGCTCACACGTTTCGGAGGG 300  
Db 301 GAAGATTTTGGATGATTTCTCTCAACAGAGTAACAGTGGCTCATAGTTTCGGAGGG 360  
QY 301 GGGACCAAGTGGAAATTA 320  
Db 361 GGGACCAAGTGGAAATAA 380

RESULT 5  
US-08-484-537-82  
; Sequence 82, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Townsend and Townsend Khourie and Crew  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-484-537-82

Query Match 77.3%; Score 248; DB 4; Length 381;  
Best Local Similarity 85.9%; Pred. No. 2.9e-70;

Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
QY 1 GAGATGTGCTAACTCAGTCTCAGCCAGCCCTGCTCTCAGCCAGGAGAAAGGGGAGCT 60  
Db 61 GATATTGTGCTAACTCAGTCTCAGCCAGCCCTGCTCTCAGCCAGGAGATACGGTCAGT 120  
QY 61 CTTTCTCGCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120  
Db 121 CTTTCTCGCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 180  
QY 121 GGTCAAGCCCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180  
Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 240  
QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCCTCACTATCCTCAAGTCTGGAGCGT 240  
Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCGCTCACACGTTTCGGAGGG 300  
Db 301 GAAGATTTTGGATGATTTCTCTCAACAGAGTAACAGTGGCGCTCATAGTTTCGGAGGG 360  
QY 301 GGGACCAAGTGGAAATTA 320  
Db 361 GGGACCAAGTGGAAATAA 380

RESULT 6  
US-08-436-463-3  
; Sequence 3, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YON, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:

NAME/KEY: CDS  
LOCATION: 23..403  
US-08-436-463-3

Query Match 77.3%; Score 248; DB 1; Length 424;  
Best Local Similarity 85.9%; Pred. No. 3e-70;  
Matches 275; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCACCCCTGCTCTCAGCCCGAGGAGAAAGGCGACT 60  
DB 83 GATATTGCTAACTCAGTCTCCAGCACCCCTGCTCTGACTCCAGGAGATAGCGTCAGT 142  
QY 61 CTTTCCTGCCAGCGCCAGCAAGATATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120  
DB 143 CTTTCCTGCCAGCGCCAGCAAGATATTAGCAACAACCTACACTGCTATCAACAATCA 202  
QY 121 GGTCACGCCCAAGGCTTCATCAATGATCGTTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 203 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 262  
QY 181 AGTTTCAGTGGCAGTGCAGGACAGATTTACCTCCTCACTATCTCCAGTCTGGAGCCT 240  
DB 263 AGTTTCAGTGGCAGTGCAGGACAGATTTACCTCCTCACTATCTCCAGTCTGGAGCCT 322  
QY 241 GAAGATTTTCAGTCTTACTTGTCAACAGAGTGGCAGCTGGCCTCACAGTTCCGAGGG 300  
DB 323 GAAGATTTTGAATGATTTCTGTCAACAGATTAACAGTGGCCTCACAGTTCGGTGCT 382  
QY 301 GGGACCAAGGTGGAATTA 320  
DB 383 GGGACCAAGGTGGAATTA 402

## RESULT 7

5453363-1  
PATENT NO. 5453363  
APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF  
TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR  
ING AFTER GENETIC EXPRESSION IN PROKARYOTES  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206,044  
FILING DATE: 02-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 942,370  
FILING DATE: 09-SEP-1992  
APPLICATION NUMBER: 498,500  
FILING DATE: 23-MAR-1990  
APPLICATION NUMBER: 76,207  
FILING DATE: 23-OCT-1986  
SEQ ID NO: 1  
LENGTH: 5238

Query Match 75.3%; Score 241.6; DB 6; Length 5238;  
Best Local Similarity 84.7%; Pred. No. 8.7e-68;  
Matches 271; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCACCCCTGCTCTCAGCCCGAGGAGAAAGGCGACT 60  
DB 7 gatattgttaactcagttccagccacctgtctgtgactccaagagatagcgtcagt 66  
QY 61 CTTTCCTGCCAGCGCCAGCAAGATATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120  
DB 67 ctttcctgagggccagcagaaagtattagcaaacctacactggtatcaacaaaataca 126  
QY 121 GGTCACGCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 127 catgagttctcaaggtctctcaataatgcttccagtgccatctctg99gatccccctct 186  
QY 181 AGTTTCAGTGGCAGTGGGACAGATTTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

DB 187 aggttcagtgagtgatcagggacagatttctcactctcagtatcaacagtgtagagact 246  
QY 241 GAAGATTTTCAGTCTTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300  
DB 247 gaagattttggaatgtatttctgtcaacagagtaacagctggcctctcactcagcttgggtgct 306  
QY 301 GGGACCAAGGTGGAATTA 320  
DB 307 gggaccaaagctggagctgaa 326

## RESULT 8

US-08-232-081B-35  
Sequence 35 Application US/08232081B  
Patent No. 5886152  
GENERAL INFORMATION:  
APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIJENES, JOHN  
APPLICANT: NOGUCHI, HIROSHI  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,081B  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-232-081B-35

Query Match 70.8%; Score 227.2; DB 2; Length 321;  
Best Local Similarity 81.9%; Pred. No. 1.2e-63;  
Matches 262; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCACCCCTGCTCTCAGCCCGAGGAGAAAGGCGACT 60  
DB 1 GAGATCGTCTGACTCAGTCTCCAGGCACACTGCTCTGAGTCCAGGAGAAAGGCCACA 60  
QY 61 CTTTCCTGCCAGCGCCAGCAAGATATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120  
DB 61 CTGTCTCTGAGGCGCAGTCAACCATTTGGCAAGACATACACTGCTATCAGCAGAGACCA 120  
QY 121 GGTCACGCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 121 GGCCAGGCGCCCAAGGCTTCTCATCAAGTATGCTTCTGAGTCTATCTCTGGGATCCCTGAT 180  
QY 181 AGTTTCAGTGGCAGTGGGACAGATTTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTTACTTTACAACTCTCCAGGCTGGAGCCA 240  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTAGTAGTGGCCGCTACGTTCCGTCAG 300  
QY 301 GGGACCAAGGTGGAATAA 320  
Db 301 GGGACCAAGGTGAGATAAA 320

## RESULT 9

US-08-232-081B-36  
; Sequence 36, Application US/08232081B  
; Patent No. 5886152  
; GENERAL INFORMATION:  
; APPLICANT: NAKATANI, TOMOYUKI  
; APPLICANT: GOMI, HIDEYUKI  
; APPLICANT: WIJDNES, JOHN  
; APPLICANT: NOGUCHI, HIROSHI  
; TITLE OF INVENTION: HUMANIZED B-B10  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 20-3484  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 321 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-232-081B-36

Query Match 69.8%; Score 224; DB 2; Length 321;  
Best Local Similarity 81.2%; Pred. No. 1.2e-62;  
Matches 260; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCCCTGTCTCTCAGCCCGCAGGAGAAAGCGGACT 60  
Db 1 GAGATCGCTCTGACCTGACCTCTCCAGGCACACTGTCTCTGAGTCCAGGAGAAAGGCCACA 60  
QY 61 CTTTCCTCCAGGCCAGCAAGATATTAGCAACCACTACACTGCTATCAACAAAGGCT 120  
Db 61 CGTCTCTCAGGCCGAGTCAGACCACTTGGCAAGCATACACTGGTATCAGCAGAGCCA 120  
QY 121 GCTCAAGCCCCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCGCC 180  
Db 121 GCGCCAGGCCCGCAAGGCTTCTCATATATTATGTTCTGAGTCTATCTCTGGCATCCCTGAT 180  
QY 181 AGTTTCAGTGGCAGTGGATCAGGAGACAGATTTTCAACCCCTCACTATCTCCAGTCTGGAGCCT 240

Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTTACTTTACAACTCTCCAGGCTGGAGCCA 240  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTAGTAGTGGCCGCTACGTTCCGTCAG 300  
QY 301 GGGACCAAGGTGGAATAA 320  
Db 301 GGGACCAAGGTGAGATAAA 320

## RESULT 10

US-08-737-560A-13  
; Sequence 13, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuul  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuul  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; STREET: Kwanak-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737.560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1  
; OTHER INFORMATION: light chain variable region  
US-08-737-560A-13

Query Match 69.8%; Score 224; DB 2; Length 324;  
Best Local Similarity 81.2%; Pred. No. 1.2e-62;  
Matches 260; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCCCTGTCTCTCAGCCCGCAGGAGAAAGCGGACT 60



Db 1 GACATTGTGATGACCCAGTCTCCAGCCAGTCTGTGACTCCAGGAGATAGACTCTCT 60  
QY 61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCT 120  
Db 61 CTTTCTCCAGGCGCAGCAGTATTAGCAACCTACACTGTGTATCAACAAGGCT 120  
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 180  
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 180  
QY 181 AGGTTCAAGTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 240  
Db 181 AGGTTCAAGTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 240  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCTCAGCTCTGGAGCT 300  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCTCAGCTCTGGAGCT 300  
QY 301 GGCACCAAGCTGGAAATCAA 320  
Db 301 GGCACCAAGCTGGAAATCAA 320

## RESULT 11

US-08-737-560A-8  
: Sequence 8, Application US/08737560A  
: Patent No. 5928893  
: GENERAL INFORMATION:  
: APPLICANT: KANG, Chang-Yuil  
: APPLICANT: KIM, Joong-Gon  
: TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
: TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
: NUMBER OF SEQUENCES: 13  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: KANG, Chang-Yuil  
: STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
: STREET: Kwanak-gu  
: CITY: Seoul  
: STATE: Seoul  
: COUNTRY: Republic of Korea  
: ZIP: 151-057  
: ADDRESSEE: KIM, Joong-Gon  
: STREET: Hanyang Apt. 72-1213, Apjung-dong, Kangnam-gu  
: CITY: Seoul  
: STATE: Seoul  
: COUNTRY: Republic of Korea  
: ZIP: 135-110  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
: COMPUTER: IBM PC/AT  
: OPERATING SYSTEM: MS-DOS  
: SOFTWARE: Word Perfect 5.1  
: CURRENT APPLICATION DATA: US/08737,560A  
: APPLICATION NUMBER: 08-APR-1995  
: FILING DATE: 13-NOV-1996  
: CLASSIFICATION: 536  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: KR 95-8176  
: FILING DATE: 08-APR-1995  
: ATTORNEY/AGENT INFORMATION:  
: NAME:  
: REGISTRATION NUMBER:  
: REFERENCE/DOCKET NUMBER:  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE:  
: TELEFAX:  
: INFORMATION FOR SEQ ID NO: 8:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 363 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear

: MOLECULE TYPE: DNA  
: FEATURE:  
: OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain  
: OTHER INFORMATION: variable region  
: OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1  
: OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2  
: OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3  
: OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region  
US-08-737-560A-8

Query Match 69.8%; Score 224; DB 2; Length 363;  
Best Local Similarity 81.2%; Pred. No. 1.3e-62;  
Matches 260; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCAGCTCTCTCAGCCAGGAGAAAGGCGCT 60  
Db 1 GACATTGTGATGACCCAGTCTCCAGCCAGTCTGTGACTCCAGGAGATAGACTCTCT 60  
QY 61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCT 120  
Db 61 CTTTCTCCAGGCGCAGCAGTATTAGCAACCTACACTGTGTATCAACAAGGCT 120  
QY 121 GGTCAAGCCCAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 180  
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 180  
QY 181 AGGTTCAAGTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 240  
Db 181 AGGTTCAAGTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCGGGATCCCGCC 240  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCTCAGCTCTGGAGCT 300  
Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCTCAGCTCTGGAGCT 300  
QY 301 GGCACCAAGCTGGAAATCAA 320  
Db 301 GGCACCAAGCTGGAAATCAA 320

## RESULT 12

US-08-476-176B-3  
: Sequence 3, Application US/08476176B  
: Patent No. 5958708  
: GENERAL INFORMATION:  
: APPLICANT: Hardman, No. 5958708man  
: APPLICANT: Kolbinger, Frank  
: APPLICANT: Saldanha, Jose  
: TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
: TITLE OF INVENTION: Immunoglobulin isotype  
: NUMBER OF SEQUENCES: 55  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: No. 5958708artis Patent Department  
: STREET: 59 Route 10  
: CITY: East Hanover  
: STATE: New Jersey  
: COUNTRY: USA  
: ZIP: 07936-1080  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/476,176B  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/127,721  
: FILING DATE: 27-SEPTEMBER-1993  
: APPLICATION NUMBER: US 07/952,802  
: FILING DATE: 25-SEPTEMBER-1992  
: ATTORNEY/AGENT INFORMATION:



STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07936-1080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,246A  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/127,721  
 FILING DATE: 27-SEPTEMBER-1993  
 APPLICATION NUMBER: US 07/952,802  
 FILING DATE: 25-SEPTEMBER-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 6072035ak, Henry P.  
 REGISTRATION NUMBER: 33,200  
 REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 277-5110  
 TELEFAX: (908) 277-4306  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 322 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..321  
 OTHER INFORMATION: /product= "light chain variable  
 OTHER INFORMATION: domain of murine antibody TES-C21"  
 US-08-485-246A-3

Query Match 67.3%; Score 216; DB 3; Length 322;  
 Best Local Similarity 79.7%; Pred. No. 4.5e-60;  
 Matches 255; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60  
 Db 1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAAGTCACT 60

Qy 61 CTTTCCTCCAGGCGCAGCAAGTATTAGCAACCACTTACACTGGTATCAACAAGGCT 120  
 Db 61 TTCTCTCGAGGCGCAGTCAAGTATTGGCACAACATACACTGGTATCAACAAGAAACA 120

Qy 121 GGTCAGCCCCAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180  
 Db 121 GATGGTCTCCAAAGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCC 180

Qy 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240  
 Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTACTCTAAACATCAACAGTGTGGAGTCT 240

Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTTCACACGTTCCGAGGG 300  
 Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTATAGTGGCCAAACACCGTTCCGAGGG 300

Qy 301 GGGACCAAGTGGAAATTA 320  
 Db 301 GGGACCAAGCTGGAGATAAA 320

RESULT 15  
 US-08-232-081B-39  
 ; Sequence 39, Application US/08232081B  
 ; Patent No. 5886152  
 ; GENERAL INFORMATION:

APPLICANT: NAKATANI, TOMOYUKI  
 APPLICANT: GOMI, HIDEYUKI  
 APPLICANT: WIJDENES, JOHN  
 APPLICANT: NOGUCHI, HIROSHI  
 TITLE OF INVENTION: HUMANIZED B-B10  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
 STREET: PO BOX 747  
 CITY: FALLS CHURCH  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22040-0747  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/232,081B  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SVENSSON, LEONARD R  
 REGISTRATION NUMBER: 30,330  
 REFERENCE/DOCKET NUMBER: 20-3484  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 205-8000  
 TELEFAX: (703) 205-8050  
 INFORMATION FOR SEQ ID NO: 39:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 321 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..321  
 US-08-232-081B-39

Query Match 64.3%; Score 206.4; DB 2; Length 321;  
 Best Local Similarity 77.8%; Pred. No. 5.2e-57;  
 Matches 249; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60  
 Db 1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAAGTCACT 60

Qy 61 CTTTCCTCCAGGCGCAGCAAGTATTAGCAACCACTTACACTGGTATCAACAAGGCT 120  
 Db 61 TTCTCTCGAGGCGCAGTCAAGTATTGGCACAACATACACTGGTATCAAGGAAGAACA 120

Qy 121 GGTCAGCCCCAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCCGCC 180  
 Db 121 AATGGTCTCCAAAGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCC 180

Qy 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240  
 Db 181 AGGTTAGTGGCAGTGGATCAGGACAGATTTACTCTTAGCATCAACAGTGTGGAGTCT 240

Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTTCACACGTTCCGAGGG 300  
 Db 241 GAAGATTTTGCAGTCTATTACTGTCAACAAAGTATAGTGGCCCGCTCACGTTCCGAGGG 300

Qy 301 GGGACCAAGTGGAAATTA 320  
 Db 301 GGGACCAAGCTGGAGCTGAA 320

Search completed: October 11, 2001, 15:14:14

Job time: 5001 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:02:35 ; Search time 31.63 seconds  
(without alignments)  
257.688 Million cell updates/sec

Title: US-08-791-391A-4  
Perfect score: 561  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQQSGSWPHTFGGKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	469	83.6	144	2 PL0106	Ig kappa chain pre
2	459	81.8	111	2 S23628	Ig kappa chain v r
3	457	81.5	128	2 A56701	Ig kappa chain v r
4	456	81.3	128	2 S40379	Ig kappa chain v-J
5	453	80.7	107	2 B45722	anti-glycoprotein
6	451.5	80.5	114	2 S54905	Ig kappa chain v r
7	450	80.2	108	2 G44151	Ig kappa chain v r
8	448	79.9	123	2 S35479	Ig kappa chain pre
9	447	79.7	107	2 A45722	anti-glycoprotein
10	446	79.5	106	2 FC4282	Ig kappa chain (an
11	443	79.0	117	2 S40362	Ig kappa chain - h
12	442	78.8	106	2 PL0267	Ig kappa chain v r
13	442	78.8	125	2 A30344	Ig kappa chain v-J
14	439.5	78.3	109	2 A30608	Ig kappa chain v-I
15	439	78.3	129	2 S29627	Ig kappa chain v r
16	437	77.9	128	2 S40345	Ig kappa chain v-J
17	436	77.7	107	2 S34005	Ig kappa chain v r
18	433.5	77.3	129	2 A32274	Ig kappa chain pre
19	432.5	77.1	108	2 B30608	Ig kappa chain v-I
20	431.5	76.9	109	2 G30607	Ig kappa chain v-I
21	430.5	76.7	109	1 K3HU71	Ig kappa chain v-I
22	430	76.6	107	2 S57444	Ig kappa chain v-J
23	429.5	76.6	109	2 D30601	Ig kappa chain v-I
24	429.5	76.6	109	2 C30601	Ig kappa chain v-I
25	428.5	76.4	109	2 H30601	Ig kappa chain v-I
26	428	76.3	128	2 S40343	Ig kappa chain v-J
27	427.5	76.2	109	1 K3HU51	Ig kappa chain v-I
28	426.5	76.0	109	2 B30601	Ig kappa chain v-I
29	426.5	76.0	109	2 B30601	Ig kappa chain v-I

ALIGNMENTS

RESULT 1

PL0106

Ig kappa chain precursor V-J-C region (L51) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C;Accession: PL0106

R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A;Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A;Reference number: PL0106; MUID:89235583

A;Accession: PL0106

A;Molecule type: mRNA

A;Residues: 1-144 <SL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-115/Domain: V region <VRE>

F;36-110/Domain: immunoglobulin homology <IMM>

F;44-54/Region: complementarity-determining 1

F;70-76/Region: complementarity-determining 2

F;109-115/Region: complementarity-determining 3

F;116-127/Domain: J region <JRG>

F;128-144/Domain: C region (fragment) <CRE>

Query Match 83.6%; Score 469; DB 2; Length 144;

Best Local Similarity 85.0%; Pred. No. 1.9e-34;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSQASQISNHLHWYQORPGQAPRLLIKYSQSIGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSQASQISNHLHWYQORPGQAPRLLIKYSQSIGIPA 80

QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKVEIK 107

Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYCCQSGSWPHTFGGKVEIK 127

RESULT 2

S23628

Ig kappa chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C;Accession: S23628

R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A

J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A;Reference number: S23623; MUID:92156804

A;Accession: S23628

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-111 <OLE>

A:Cross-references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 459; DB 2; Length 111;  
Best Local Similarity 83.2%; Pred. No. 1.le-33;  
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYKRSQISGIPA 60

Db 1 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYDASNRATGIPA 60

QY 61 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 107

Db 61 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 107

#### RESULT 3

A56701

Ig kappa chain V region precursor (HuA) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jan-2000

C:Accession: A56701

R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.

J. Biol. Chem. 270, 12457-12465, 1995

A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are new

A:Reference number: A56701; MUID:95279371

A:Accession: A56701

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <NIC>

A:Cross-references: GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:g762824

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 457; DB 2; Length 128;  
Best Local Similarity 82.2%; Pred. No. 2e-33;  
Matches 88; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYKRSQISGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYDASNRATGIPA 80

QY 61 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 107

Db 81 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 127

#### RESULT 4

S40379

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40379

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891

A:Accession: S40379

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-128 <KLE>

A:Cross-references: EMBL:X72489; NID:g441446; PIDN:CAA51157.1; PID:g441447

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 456; DB 2; Length 128;

Best Local Similarity 81.3%; Pred. No. 2.4e-33;  
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYKRSQISGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYASNRATGIPA 80  
QY 61 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 107  
Db 81 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 127

#### RESULT 5

B45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C:Accession: B45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va

J. Virol. 67, 489-496, 1993

A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on

A:Reference number: A45722; MUID:93100833

A:Accession: B45722

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-107 <SIM>

A>Note: sequence extracted from NCBI backbone (NCBIP:120590)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: glycoprotein

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 453; DB 2; Length 107;  
Best Local Similarity 76.6%; Pred. No. 3.7e-33;  
Matches 82; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYKRSQISGIPA 60

Db 1 DIVLTQSPATLSVTPGDSVSLSCASQSTNSHLHWYQORPGQAPRLLIYKRSQISGIPS 60

QY 61 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 107

Db 61 RFSGSGGTDFLTITSSLEPEDFAVYVCOQSGSWPHTFGGKVEIK 107

#### RESULT 6

S54905

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C:Accession: S54905

R:Esposito, G.; Traboni, C.

submitted to the EMBL Data Library, November 1994

A:Description: Cloning and sequencing of cDNA coding for the variable domains of a hu

A:Reference number: S54905

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-114 <ESP>

A:Cross-references: EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PID:g809555

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 451.5; DB 2; Length 114;  
Best Local Similarity 80.6%; Pred. No. 5.3e-33;  
Matches 87; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYKRSQISGIPA 60

Db 1 DVVMTQSPATLSLSPGERATLSCQASQSTNSHLHWYQORPGQAPRLLIYDASRRATGIPA 60

QY 61 RFSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 107  
|||||  
Db 61 RFSGSGGDTFTLTISSELEDFAVYCCQSGSWPHPLTFGGGKVEIK 108

RESULT 7  
G44151  
Ig kappa chain V region (JM-10) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C:Accession: G44151  
R:Zebende, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pya  
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
A:Reference number: A44151; MUID:92228746  
A:Accession: G44151  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-108 <MEM>  
A:Cross-references: GB:M88317; NID:g183968; PIDN:AAA35975.1; PID:g183969  
A:Note: nucleotide translation not given  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 450; DB 2: Length 108;  
Best Local Similarity 82.7%; Pred. No. 6.8e-33;  
Matches 86; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
QY 4 LTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPARFS 63  
|||||  
Db 3 LTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPARFS 62  
|||||  
QY 64 GSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 107  
|||||  
Db 63 GSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 106

RESULT 8  
S35479  
Ig kappa chain precursor V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: S35479  
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.  
Nucleic Acids Res. 20, 4099, 1992  
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m  
A:Reference number: S35479; MUID:92375706  
A:Accession: S35479  
A:Molecule type: DNA  
A:Residues: 1-123 <TAK>  
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148  
C:Genetics:  
A:Map position: 6  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 448; DB 2: Length 123;  
Best Local Similarity 75.7%; Pred. No. 1.2e-32;  
Matches 81; Conservative 18; Mismatches 8; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPA 60  
|||||  
Db 13 DIVLTQSPATLSVTPGKVSLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 72  
|||||  
QY 61 RFSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 107  
|||||

Db 73 RFSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKLEIK 119

RESULT 9  
A45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (A  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: A45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on  
A:Reference number: A45722; MUID:93100833  
A:Accession: A45722  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 447; DB 2: Length 107;  
Best Local Similarity 74.8%; Pred. No. 1.2e-32;  
Matches 80; Conservative 18; Mismatches 9; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPA 60  
|||||  
Db 1 DIVLTQSPATLSVTPGKVSLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPS 60  
|||||  
QY 61 RFSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 107  
|||||  
Db 61 RFSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKLEIK 107

RESULT 10  
PC4282  
Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 21-Jan-2000  
C:Accession: PC4282; PC4284  
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.  
Biochem. Biophys. Res. Commun. 232, 101-106, 1997  
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltra  
A:Reference number: PC4279; MUID:97236289  
A:Accession: PC4282  
A:Molecule type: protein  
A:Residues: 1-106 <SUZ>  
A:Note: E-42  
A:Accession: PC4284  
A:Molecule type: protein  
A:Residues: 1-106 <SUZ>  
A:Note: E-56  
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sj  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 446; DB 2: Length 106;  
Best Local Similarity 81.0%; Pred. No. 1.5e-32;  
Matches 85; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPATLSLSPGRATLSQASQISNHLHWYQORPCQAPRLTIKYRSQISGIPARF 62  
|||||  
Db 1 VLTQSPATLSLSPGRATLSQASQISNHLHWYQKSHSPRLTIKYRSQISGIPAKF 60  
|||||  
QY 63 SGSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 107  
|||||  
Db 61 SGSGSGGDTFTLTISSELEDFAVYCCQSGSWPH-TFGGKVEIK 105

RESULT 11







**THIS PAGE BLANK (USPTO)**



OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 RT group";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 CC GLOBULIN ACTIVITY.  
 DR PIR; A01892; K3HUSI.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89  
 FT NON\_TER 109 109  
 FT SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;  
 SQ  
 Query Match 76.2%; Score 427.5; DB 1; Length 109;  
 Best Local Similarity 79.6%; Pred. No. 5.2e-37;  
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 EIVLTSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQISGIP 59  
 Db 1 EIVLTSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQISGIP 59  
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 107  
 Db 61 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 108  
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 107  
 Db 61 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 108  
 RESULT 3  
 KV3L\_HUMAN STANDARD; PRT; 129 AA.  
 ID KV3L\_HUMAN  
 AC P18135;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88171307; PubMed=3127527;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene  
 RT expressed in chronic lymphocytic leukemia with little or no somatic  
 RT mutation. Implications for etiology and immunotherapy";  
 RL J. Exp. Med. 167:840-852(1988).  
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
 CC LEUKEMIA.  
 DR PIR; P10022; K3HUHA.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.  
 FT DOMAIN 21 43 FRAMEWORK 1  
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 56 70 FRAMEWORK 2.  
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 78 109 FRAMEWORK 3.  
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 119 129 JK1 SEGMENT.  
 FT DISULFID 43 109  
 BY SIMILARITY.

FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;  
 Query Match 76.0%; Score 426.5; DB 1; Length 129;  
 Best Local Similarity 79.6%; Pred. No. 8e-37;  
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 EIVLTSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQISGIP 59  
 Db 21 EIVLTSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQISGIP 59  
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 107  
 Db 81 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 128  
 RESULT 4  
 KV3E\_HUMAN STANDARD; PRT; 109 AA.  
 ID KV3E\_HUMAN  
 AC P01623;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION WOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 RT group";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 CC GLOBULIN ACTIVITY.  
 DR PIR; A01896; K3HUSL.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89  
 FT NON\_TER 109 109  
 FT SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;  
 SQ  
 Query Match 75.1%; Score 421.5; DB 1; Length 109;  
 Best Local Similarity 79.6%; Pred. No. 2.1e-36;  
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;  
 QY 1 EIVLTSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQISGIP 59  
 Db 1 EIVLTSPATLSLSPGERATLSCQASQISN-HLHWYQQRPGQAPRLLIKYRSQISGIP 59  
 QY 60 ARFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 107  
 Db 61 DRFSGSGGTDFLTITSLRLEPDAFVAVYCOQGSWPHFTGGGKVEIK 108  
 RESULT 5  
 KV3M\_HUMAN STANDARD; PRT; 129 AA.  
 ID KV3M\_HUMAN  
 AC P18136;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.



```
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 73.4%; Score 412; DB 1; Length 115;
Best Local Similarity 83.2%; Pred. No. 2.1e-35;
Matches 79; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
    |||||
DB 21 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 80
    |||||
QY 61 RFSGSGGTFTLTISLLEPEFAVYCCQSGSWP 95
    |||||
DB 81 RFSGSGGTFTLTISLLEPEFAVYCCQSGSWP 115
    |||||

RESULT 8
KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN V-III REGION POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
    from two idiotypically cross reactive Igm anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
    GLOBULIN ACTIVITY.
DR PIR: A01897; K3HUPM.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8A86 CRC64;

Query Match 73.0%; Score 409.5; DB 1; Length 109;
Best Local Similarity 75.0%; Pred. No. 3.6e-35;
Matches 81; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISN-HLHWYQORPGQAPRLLIKYRSQISGIP 59
    |||||
DB 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIP 60
    |||||
QY 60 ARFSGSGGTFTLTISLLEPEFAVYCCQSGSWPHTFGGKVEIK 107
    |||||
DB 61 ARFSGSGGTFTLTISLLEPEFAVYCCQSGSWPHTFGGKVEIK 108
    |||||

RESULT 9
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
    III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.9%; Score 409; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 4.8e-35;
Matches 80; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60
    |||||
DB 21 EIVLTQSPATLSLSPGERATLSCAQSQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 80
    |||||
QY 61 RFSGSGGTFTLTISLLEPEFAVYCCQSGSWPHTFGGKVEIK 107
    |||||
DB 81 RFSGSGGTFTLTISLLEPEFAVYCCQSGSWPHTFGGKVEIK 127
    |||||

RESULT 10
KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
    of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3HUB6.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
```

```
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 72.3%; Score 405.5; DB 1; Length 108;
Best Local Similarity 73.1%; Pred. No. 9.1e-35;
Matches 79; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQIS-NHLHWYQORPGQAPRLLIKYSQISGIP 59
DB 1 ZIVLTZSPGTLSPGZRAALSCRAQSLSGNYLAWYQKFGQAPRLLIYGVSSRATGIP 60

QY 60 ARFGSGSGTDTLTISLLEPEDFAVYCCQSGSWPHTFGGKVEIK 107
DB 61 DRFGSGSGADFTLTISRLEPEDFAVYCCQYSGSPFTFGGSKLEIK 108

RESULT 11
KVLM_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR: A01893; K3HUGO.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11630 MW; 9349A5BID93588B6 CRC64;

Query Match 71.6%; Score 401.5; DB 1; Length 109;
Best Local Similarity 75.9%; Pred. No. 2.3e-34;
Matches 82; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQAS-OSISNHLHWYQORPGQAPRLIKYSQISGIP 59
DB 1 EIVLTQSPGTLSPGERATLSCRAALSSRGYLAWYQKFGQAPRLLIYGVSSRATGIP 60

QY 60 ARFGSGSGTDTLTISLLEPEDFAVYCCQSGSWPHTFGGKVEIK 107
DB 61 DRFGSGSGADFTLTISRLEPEDFAVYCCQYSGSPRSGGKVEIK 108

RESULT 12
KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KLHULY.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 67.6%; Score 379; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 4.5e-32;
Matches 68; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIKYSQISGIP 60
DB 1 DIQMTQSPSSLSVSGDVRVITCQASQNVNAYLNWYQKPGPLKLLIYGASTREAGVPS 60

QY 61 RFSGSGGTDTLTITISLLEPEDFAVYCCQSGSWPHTFGGKVEIK 107
DB 61 RFSGSGGTDTLTITISLLEPEDFAVYCCQYNNWPPFTFGGKVEIK 107

RESULT 13
KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01868; KLHULH.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
SQ SEQUENCE 24 34
```

```

QY      56 SCIPARFSGSGSDTFTLTISSELPEDFAVYYCQSGSWPHTFGGTVKEIK 107
        ||||||| ||||| : | | ||||| |:|||||:||
Db      60 SCIPARFSGSGRTDFTLTINPEADVATYYCQGSNEDPYTFGGTKLEIK 111
        ||||||| ||||| : | | ||||| |:|||||:||

RESULT 15
KV5I_MOUSE
ID   KV5I_MOUSE          STANDARD;             PRT;       115 AA.
AC   P01642;
DT   21-JUL-1986 (Rel. 01, Created)
DI   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
CC   -!- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE junctions
CC   THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC   LACKING RESIDUES 17-19.
DR   PIR: A01925; KVMSL7.
DR   InterPro: IPR003006; -.
DR   Pfam: PF00047; Ig; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL              1     20
FT   CHAIN               21    >115  IG KAPPA CHAIN V-V REGION L7.
FT   DOMAIN              21    43     FRAMEWORK 1.
FT   DOMAIN              44    54     COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN              55    69     FRAMEWORK 2.
FT   DOMAIN              70    76     COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN              77    108    FRAMEWORK 3.
FT   DOMAIN              109   >115  COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID            43    108    BY SIMILARITY.
FT   NON_TER             115   115
SQ   SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match           66.1%; Score 371; DB 1; Length 115;
Best Local Similarity 72.6%; Pred. No. 3.2e-31;
Matches 69; Conservative 12; Mismatches 14; Indels 0; Gaps 0

Qy      1 EIVLTQSPATLSLPGGERATLSQASQISNHLHWYQPCGPAGPRLTIKYRSQSIGIPA 60
        ||||||| ||||| : | | ||||| ||||| :|||||:|||||:
Db      21 DILTQSPAIISSVPGERVFSCRASQSIGTSHWYQQTNGSPRLLIKYASESISGPS 80
        ||||||| ||||| : | | ||||| ||||| :|||||:|||||:

Qy      61 RFSGSGSDTFTLTISSELPEDFAVYYCQSGSWP 95
        ||||||| ||||| : | | ||||| ||||| :|||||:|||||:
Db      81 RFSGSGSDTFTLTINSVESEADIADYYCQGSNSWP 115
        ||||||| ||||| : | | ||||| ||||| :|||||:|||||:

Search completed: October 11, 2001, 12:08:43
Job time: 403 sec

```





**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:07:34 ; Search time 46.3 Seconds  
(without alignments)  
305.759 Million cell updates/sec

Title: US-08-791-391A-4

Perfect score: 561

Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQSGSWPHFTGGTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:\*\*

1: sp\_archaea:\*\*

2: sp\_bacteria:\*\*

3: sp\_fungi:\*\*

4: sp\_human:\*\*

5: sp\_invertebrate:\*\*

6: sp\_mammal:\*\*

7: sp\_mhc:\*\*

8: sp\_organelle:\*\*

9: sp\_phase:\*\*

10: sp\_plant:\*\*

11: sp\_rodent:\*\*

12: sp\_unclassified:\*\*

13: sp\_vertebrate:\*\*

14: sp\_virus:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	428.5	76.4	109	4 Q9UL85	Q9ul85 homo sapien
2	427	76.1	108	4 Q9UL83	Q9ul83 mus sapien
3	426.5	76.0	109	4 Q9UL78	Q9ul78 homo sapien
4	401.5	71.6	109	4 Q9UL86	Q9ul86 homo sapien
5	384	68.4	108	4 Q9UL77	Q9ul77 mus sapien
6	371	66.1	108	4 Q9UL79	Q9ul79 homo sapien
7	365	65.1	108	4 Q9UL70	Q9ul70 homo sapien
8	361.5	64.4	107	4 Q9UL81	Q9ul81 mus sapien
9	337.5	60.2	106	5 Q9UL10	Q9ul10 schistosoma
10	333	59.4	99	11 Q9JL74	Q9j174 mus musculus
11	333	59.4	107	11 Q9JL84	Q9j184 mus musculus
12	332	59.2	298	11 Q9QYF0	Q9qyf0 mus musculus
13	330	58.8	214	11 Q9JL85	Q9j185 mus musculus
14	325	57.9	101	11 Q9JL78	Q9j178 mus musculus
15	314	56.0	107	11 Q9ERZ9	Q9erz9 mus musculus
16	313	55.8	103	11 Q9JL80	Q9j180 mus musculus
17	308	54.9	97	11 Q9JL76	Q9j176 mus musculus
18	308	54.9	114	4 Q9UL80	Q9ul80 homo sapien
19	306.5	54.6	104	11 Q9JL82	Q9j182 mus musculus

20	280	49.9	109	6 Q9NOW5	Q9n0w5 oryctolagus
21	235	41.9	107	4 Q9UL82	Q9ul82 homo sapien
22	216.5	38.6	107	4 Q9NSD6	Q9nsd6 homo sapien
23	182.5	32.5	109	11 Q9ETI3	Q9eti3 mus musculus
24	167	29.8	130	4 Q9NP29	Q9np29 homo sapien
25	154.5	27.5	135	4 Q9H5Z4	Q9h5z4 homo sapien
26	150	26.7	93	4 Q9UL76	Q9ul76 homo sapien
27	145	25.8	123	11 Q61243	Q61243 mus musculus
28	134	23.9	168	4 Q9UQ56	Q9uq56 homo sapien
29	126	22.5	342	13 Q9IB00	Q9ib00 spherooides
30	124.5	22.2	334	13 Q9IB05	Q9ib05 spherooides
31	123.5	22.0	331	13 Q9IB07	Q9ib07 spherooides
32	121.5	21.7	509	11 Q08907	Q08907 mus musculus
33	121.5	21.7	509	11 Q9WTN4	Q9wtm4 mus musculus
34	120	21.4	100	6 Q77624	Q77624 bos taurus
35	118	21.0	152	13 Q9YH11	Q9yhl1 ginglymosto
36	117	20.9	122	4 Q9UL84	Q9ul84 homo sapien
37	116	20.7	340	13 Q9IAZ6	Q9iaz6 spherooides
38	115.5	20.6	109	11 Q9JL75	Q9j175 mus musculus
39	115.5	20.6	509	11 Q9QX57	Q9qx57 mus musculus
40	115.5	20.6	513	11 P97797	P97797 mus musculus
41	115	20.5	100	13 Q9YH19	Q9yhi9 ginglymosto
42	114.5	20.4	119	4 Q9UL94	Q9ul94 homo sapien
43	114.5	20.4	340	13 Q9IAZ0	Q9iaz0 spherooides
44	113.5	20.2	113	4 Q9UL90	Q9ul90 homo sapien
45	113	20.1	136	13 Q9YHR9	Q9yhr9 ginglymosto

#### ALIGNMENTS

```

RESULT 1
Q9UL85 PRELIMINARY; PRT; 109 AA.
ID Q9UL85
AC Q9UL85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035029; AAD56265.1; -
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACCC CRC64;

```

```

Query Match 76.4%; Score 428.5; DB 4; Length 109;
Best Local Similarity 78.7%; Pred. No. 2.1e-40;
Matches 85; Conservative 10; Mismatches 12; Indels 1; Gaps 1;
Oy 1 EIVLTQSPATLSLSPGERATLSQASQSTSNLHWYQQQPGQPRLILKYRSQTSIGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSQASQSTSNLHWYQQQPGQPRLILKYRSQTSIGIPA 60
Oy 61 RFSGSGSTDFLTITSLLEPEDFAVYQQSGSWPH-TFGGKVEIK 107

```

RESULT	3	
Q9UL78		
ID	Q9UL78	PRELIMINARY; PRT; 109 AA.
AC	Q9UL78;	
DT	01-MAY-2000	(TEMBLrel. 13, Created)
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)
DT	01-MAR-2001	(TEMBLrel. 16, Last annotation update)
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).	
OS	Homo sapiens	(Human).
OC	Eukaryota;	Metazoa;
OC	Mammalia;	Eutheria;
OC	Primates;	Catarrhini;
OX	NCBI_TaxID=9606;	Hominidae; Homo.
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98277139;	PubMed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L.,	Kallis N.N., Berney S.M.,
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";	
RL	Clin. Immunol. Immunopathol.	87:184-192(1998).
CC	-1*- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
CC	EMBL; AF035036;	RA056272.1; -
DR		

Query Match	71.6%	Score	401.5	DB	4	Length	109
Best Local Similarity	76.9%	Pred. No.	2.1e-37				
Matches	83	Conservative	7	Mismatches	17	Indels	1
Gaps	1						
Qy	1	EIVTQSPATLSLSPGERATISCSQASQI-SNHLLHWYQORPQAPRLLIKYRSQISGIP	59				
Db	1	EIVTQSPGTLSPGERATLSCRASQVSSSYLAWYQOKPQAPRLLIYGTSSRATGIP	60				
Qy	60	ARFGSGSGTFTLTISLLEPDAFVYYCQSGSGWPHFTGGGKVKYK	107				
Db	61	DRFGSGSGTFTLTISLLEPDAFVYYCQSGSGIFFTGCTKVDIK	108				

RESULT 5  
Q9UL77  
ID Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;

```
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 68.4%; Score 384; DB 4; Length 108;
Best Local Similarity 69.2%; Pred. No. 1.9e-35;
Matches 74; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIKYSQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITCRASQGISNLYNQPKGKAPNLLIYAASLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTSSLEPEDFVAVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFSGSGSGTDFTLTSSLPEDFATVYCOQYSYSTWTEGKVEIK 107

RESULT 6
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match 65.1%; Score 365; DB 4; Length 108;
Best Local Similarity 64.5%; Pred. No. 2.5e-33;
Matches 69; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIKYSQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITCRASQGISNLYNQPKGKAPNLLIYAASLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTSSLEPEDFVAVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFSGSGSGTDFTLTSSLPEDVAVYCOQYNSAPRTFGPGKLEIK 107

RESULT 8
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
Query Match 66.1%; Score 371; DB 4; Length 108;
Best Local Similarity 67.3%; Pred. No. 5.4e-34;
Matches 72; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIKYSQSISGIPA 60
Db 1 DIVMTQSPSLLSASTGDRVTISCRMSQGISNLYNQPKGKAPNLLIYAASLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTSSLEPEDFVAVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFSGSGSGTDFTLTSSLPEDFATVYCOQYSFPTFGGKVEIK 107

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;

Query Match 65.1%; Score 365; DB 4; Length 108;
Best Local Similarity 64.5%; Pred. No. 2.5e-33;
Matches 69; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIKYSQSISGIPA 60
Db 1 DIQMTQSPSSLSASVGRVITCRASQGISNLYNQPKGKAPNLLIYAASLSQGVPS 60
Qy 61 RFSGSGSGTDFTLTSSLEPEDFVAVYCOQSGSWPHTFGGKVEIK 107
Db 61 RFSGSGSGTDFTLTSSLPEDVAVYCOQYNSAPRTFGPGKLEIK 107

RESULT 8
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```





QY 10 TSLSPGERATLSQASQSI-SNHLHWYQORPGQAPRLLIKYRSQISGIPARFSGSG 68  
Db 2 TMAASPEKITITCSASSISSNYLHWYQKPGFSPKLLIYRTSNLASGVPTFRSGSG 61  
QY 69 TDTLTITSSLEPEDFAVYCYQSGSWP-WTFGGGKVEIK 107  
Db 62 TSYSLTIGTMEADVATYCYQSGSIPRYTFGGGKLEIK 101

## RESULT 15

O9ERZ9  
ID Q9ERZ9 PRELIMINARY; PRT; 107 AA.  
AC Q9ERZ9;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
RT "Cloning and sequencing of the light chain fragment of variable region  
RT genes of an anti-hTNF-a monoclonal antibody.";  
RL J. Cell. Mol. Immunol. 12:21-26(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RT "Construction and sequencing of the single-chain antibody gene of a  
RT human TNF-alpha specific monoclonal antibody.";  
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF262753; AAG23804.1; -.  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 56.0%; Score 314; DB 11; Length 107;  
Best Local Similarity 54.2%; Pred. NO. 1.2e-27;  
Matches 58; Conservative 22; Mismatches 21; Indels 6; Gaps 1;

QY 4 LTQSPATLSLSPGERATLSQASQSI-----SNHLHWYQORPGQAPRLLIKYRSQISG 57  
Db 1 MTQSPSLAMSVGKVTMSCKSSQSVLNSNTQKNYLAWYQKPGQSPPELLVYFASTRESG 60  
QY 58 IPARFSGSGSGTDTLTITSSLEPEDFAVYCYQSGSWPHTFGGKTV 104  
Db 61 VPDREMGSGSGTDTLTITSSVQTDLADYFCQGHYRTPTFGSGTKL 107

Search completed: October 11, 2001, 12:07:34  
Job time: 409 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:57 ; Search time 44.8 Seconds  
(without alignments)  
144.794 Million cell updates/sec

Title: US-08-791-391a-4

Perfect score: 561

Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQGSMPHTFGSGTKRVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	19 AAW76002	Vitaxin antibody 1
2	561	100.0	107	22 AAB61360	Vitaxin light chain
3	555	98.9	107	19 AAW76006	LM609 grafted anti
4	555	98.9	107	22 AAB61364	Light chain variab
5	512	91.3	107	13 AAR25729	Humanised VL regio
6	512	91.3	107	22 AAB69678	Humanised CMV5 ant
7	512	91.3	107	22 AAB69690	Human Wol antibody
8	510	90.9	107	20 AAW84098	Humanised anti-alp
9	510	90.9	112	20 AAW84100	Vitronectin alpha-
10	507	90.4	127	18 AAW08946	Kappa light chain
11	501	89.3	107	18 AAW08948	Kappa light chain

12	494	88.1	107	18 AAW08949	Kappa light chain
13	490	87.3	127	21 AAY32407	Mouse anti-verotox
14	489	87.2	107	20 AAY30205	The variable light
15	488	87.0	107	20 AAY30203	The variable light
16	486	86.6	127	15 AAR50192	Light chain variab
17	486	86.6	127	20 AAY26982	Light chain variab
18	484	86.3	107	14 AAR37612	HLI2R Ab L chain v
19	483	86.1	107	21 AAY71240	Humanised antibody
20	480	85.6	107	21 AAY70604	Vkappa region of h
21	480	85.6	127	15 AAR50187	Light chain variab
22	480	85.6	127	20 AAY26980	Light chain variab
23	480	85.6	245	21 AAY70605	scfv fragment of h
24	477	85.0	127	15 AAR50191	Light chain variab
25	477	85.0	127	20 AAY26981	Light chain variab
26	470	83.8	107	19 AAY76004	LM609 antibody lig
27	470	83.8	107	22 AAB61362	Antibody LM609 lig
28	459	81.8	107	21 AAY71238	Humanised antibody
29	456	81.3	105	20 AAW87456	Jk gene product.
30	456	81.3	105	20 AAW87458	Humanised anti-alp
31	455	81.1	109	20 AAY06380	Murine monoclonal
32	454	80.9	107	22 AAB66414	Human Fab clone LD
33	449.5	80.1	108	22 AAB72884	Human anti-HER2/ne
34	448.5	79.9	107	18 AAW24513	Anti-Factor-IX hum
35	447	79.7	107	22 AAB69677	Murine CMV5 antibo
36	447	79.7	127	22 AAB69687	Murine CMV5 antibo
37	445	79.3	214	20 AAY08599	Anti-human TNF-alp
38	444	79.1	127	15 AAR54093	Sequence of mouse
39	440	78.4	109	15 AAR52033	Light chain variab
40	439	78.3	349	12 AAR12128	1b1 IgG aberrant 1
41	439	78.3	401	12 AAR12129	ORF 1 of IgG light
42	439	78.3	414	12 AAR13111	1b1 IgG aberrant 1
43	439	78.3	414	12 AAR13018	1b1 IgG aberrant 1
44	437.5	78.0	109	22 AAB62756	Human HIV-1 monocl
45	437	77.9	107	14 AAR38601	HYH light chain.

#### ALIGNMENTS

RESULT 1

AAW76002  
ID AAW76002 standard; Protein; 107 AA.

XX AC AAW76002;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody light chain variable region protein fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;  
LM609; inhibitor; integrin-mediated signal transduction; treatment;  
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAW49621.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX Claim 1; Fig 1b; 129pp; English.  
 XX This sequence represents the vitaxin antibody variable light chain  
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin  
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a  
 CC ligand and thus block integrin-mediated signal transduction. This is  
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated  
 CC disease, specifically angiogenesis and restenosis (but also e.g.  
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,  
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,  
 CC osteoporosis etc.). The antibodies contain non-murine framework regions  
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity  
 CC more than 90 times greater than that of parent the parent antibody.  
 XX Sequence 107 AA;

Query Match 100.0%; Score 561; DB 19; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQQRPGQAPRLLIKYRSQISGIPA 60  
 |||||  
 Db 1 elvltqspatlsispgeratlsqasqsisnhlhwyqqrpgqaprllikyrsgisgipa 60  
 |||||

QY 61 RFGSGSGTDFTLTISLSPEDFAVYCCQSGSWPHTFGGKVEIK 107  
 |||||  
 Db 61 rfsgsgsgtdftltisslepedfavyccqsgswphtfgggtkveik 107  
 |||||

## RESULT 2

AAAB61360  
 ID AAB61360 standard; protein; 107 AA.  
 XX  
 AC AAB61360;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Vitaxin light chain variable region protein.  
 XX  
 KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 1; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX Sequence 107 AA;

Query Match 100.0%; Score 561; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQQRPGQAPRLLIKYRSQISGIPA 60  
 |||||  
 Db 1 elvltqspatlsispgeratlsqasqsisnhlhwyqqrpgqaprllikyrsgisgipa 60  
 |||||

QY 61 RFGSGSGTDFTLTISLSPEDFAVYCCQSGSWPHTFGGKVEIK 107  
 |||||  
 Db 61 rfsgsgsgtdftltisslepedfavyccqsgswphtfgggtkveik 107  
 |||||

## RESULT 3

AAW76006  
 ID AAW76006 standard; Protein; 107 AA.  
 XX  
 AC AAW76006;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 grafted antibody light chain variable region protein fragment.  
 XX  
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 49  
 FT /label= Arg, Met  
 XX  
 PN WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 DR WPI; 1998-437472/37.  
 DR N-PSDB; AAW49843.  
 XX  
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Claim 19; Fig 7; 129pp; English.  
 XX  
 CC This sequence represents a LM609 grafted antibody variable light chain  
 CC region. LM609 and the antibody vitaxin bind selectively to integrin  
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand  
 CC and thus block integrin-mediated signal transduction. This is useful in

CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX  
 SQ sequence 107 AA;

Query Match 98.9%; Score 555; DB 19; Length 107;  
 Best Local Similarity 99.1%; Pred. No. 1e-35;  
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQSISGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQSISGIPA 60  
 QY 61 RFGSGSGTDFLTITISSELPEDFVAVYCOQSGSWPHTFGGKVEIK 107  
 DB 61 RFGSGSGTDFLTITISSELPEDFVAVYCOQSGSWPHTFGGKVEIK 107

RESULT 4

AA61364  
 ID AAB61364 standard; protein; 107 AA.  
 AC AAB61364;  
 DT 03-APR-2001 (first entry)  
 DE Light chain variable region of LM609.  
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 OS Unidentified.

PN WO200078815-A1.  
 PD 28-DEC-2000.  
 PF 23-JUN-2000; 2000WO-US17454.  
 PR 24-JUN-1999; 99US-0339922.  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 PA Huse WD, Wu H;  
 PI WPI; 2001-050110/06.  
 DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX Disclosure; Fig 7; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX Sequence 107 AA;

Query Match 98.9%; Score 555; DB 22; Length 107;  
 Best Local Similarity 99.1%; Pred. No. 1e-35;  
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQSISGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQSISGIPA 60  
 QY 61 RFGSGSGTDFLTITISSELPEDFVAVYCOQSGSWPHTFGGKVEIK 107  
 DB 61 RFGSGSGTDFLTITISSELPEDFVAVYCOQSGSWPHTFGGKVEIK 107

RESULT 5

AAR25729  
 ID AAR25729 standard; Protein; 107 AA.  
 AC AAR25729;  
 DT 13-JAN-1993 (first entry)  
 XX Humanised VL region of the mouse CMV5 antibody.  
 DE Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;  
 KW GH; light chain; variable region; framework; human; Wol.  
 XX Mus musculus.

Key Location/Qualifiers  
 FH Region 24..34  
 FT /note= "CDR"  
 FT Region 50..56  
 FT /note= "CDR"  
 FT Region 89..97  
 FT /note= "CDR"  
 FT Misc-difference 49  
 FT /note= "mutated residue"

XX WO9211018-A.  
 PN 09-JUL-1992.  
 PD 19-DEC-1991; 91WO-US09711.  
 PF 19-DEC-1990; 90US-0634278.  
 PR (PROT-) PROTEIN DESIGN LABS INC.  
 PA Co MS, Coeltingh KL, Landolfi NF, Queen CL, Schneider WP;  
 PI WPI; 1992-249842/30.  
 DR New immunoglobulin(s) having murine CDRs in human framework  
 XX regions - have lower antigenicity; useful for treating e.g. HSV,  
 PT CMV, T-cell disorders, myeloid disorders and auto-immune  
 PT conditions  
 XX Claim 40; Fig 27A; 141pp; English.

CC The sequence shows the humanised mature light chain variable  
 CC region of the mouse CMV5 antibody. Murine CDRs were used  
 CC in a human Wol framework to produce a pure humanised immunoglobulin  
 CC (Ig) which is capable of binding to the GH glycoprotein of  
 CC cytomegalovirus. The Ig is non immunogenic, due to the human  
 CC framework, and has a strong affinity for its predetermined  
 CC antigen. They can be produced in large quantities via recombinant  
 CC DNA and monoclonal antibody technology. The humanised Igs may be  
 CC used alone or in combination with chemotherapeutic agents such as  
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.  
 CC See also AAR25721-32.  
 XX



QY 61 RFSGSGTDFLTITSSLEPEDFVAVYCOQSGSWPHTFGGGKVEIK 107  
|||||  
Db 61 rfsagsgtdftltisrlepedfavyycqsgswphTFGGGKVEIK 107

## RESULT 8

AAW84098  
ID AAW84098 standard; Protein; 107 AA.

XX  
AC AAW84098;

XX  
DT 15-MAR-1999 (first entry)

XX  
DE Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL.

XX  
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
KW angiogenesis; diabetic retinopathy; inflammation;  
KW macular degeneration; osteoporosis; Paget's disease;  
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
KW D12HZHC-10.

XX  
OS Homo sapiens.

OS  
Synthetic.

XX  
FH Key Location/Qualifiers

FT Region 24..34

FT /label= CDR1

FT Region 50..56

FT /label= CDR2

FT Region 89..97

FT /label= CDR3

XX  
XX WO9840488-A1.

XX  
XX 17-SEP-1998.

XX  
XX 12-MAR-1998; 98WO-US04987.

XX  
XX 12-MAR-1997; 97US-0039609.

XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX  
XX Johanson KO, Jonak ZL, Taylor AH;

XX  
XX WPI: 1999-034590/03.

XX  
XX N-PSDB; AAV71800.

XX  
XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
PT immunotherapeutic treatment of e.g. diabetic retinopathy.  
PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
PT osteoporosis

XX  
PS Claim 2; Page 61-62; 97pp; English.

XX  
XX This is the amino acid sequence of the light chain variable region  
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor  
CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence  
CC (see AAW84096) of human Kabat subgroup III kappa chain, with  
CC complementarity determining regions (CDRs) from the murine  
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody  
CC D12 (see AAW84093). 3 Murine framework residues (1, 49 and 60)  
CC are retained. The humanised light chain can be expressed in host  
CC cells using nucleic acid molecules (see AAV71800) of the invention.  
CC Humanised D12 VH is also provided (see AAW84097). The humanised  
CC antibodies can be used for passive immunotherapy of disorders  
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or  
CC angiogenic-related disorders, such as angiogenesis associated  
CC with diabetic retinopathy, atherosclerosis and restenosis, chronic  
CC inflammatory disorders, macular degeneration, rheumatoid arthritis  
CC and cancer, e.g. solid tumour metastasis, and diseases where bone  
CC resorption is associated with pathology such as osteoporosis,

CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,  
CC osteolytic lesions produced by bone metastasis, bone loss due to  
CC immobilisation or sex hormone deficiency. They can also be used for  
CC targeted drug therapy, and for detection and diagnosis.

XX  
SQ Sequence 107 AA;

Query Match 90.9%; Score 510; DB 20; Length 107;

Best Local Similarity 90.7%; Pred. No. 2.8e-32;

Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIKYSQISGIPA 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 1 divltqspgtlspsgeratlsqasqisnhlhwyyqkpgqaprlilikyasqisgips 60

QY 61 RFSGSGTDFLTITSSLEPEDFVAVYCOQSGSWPHTFGGGKVEIK 107  
|||||

Db 61 rfsagsgtdftltisrlepedfavyycqsgswphTFGGGKVEIK 107  
|||||

## RESULT 9

AAW84100  
ID AAW84100 standard; Protein; 112 AA.

XX  
AC AAW84100;

XX  
DT 15-MAR-1999 (first entry)

XX  
DE Vitronectin alpha-v beta-3 MAB VL.

XX  
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
KW angiogenesis; diabetic retinopathy; inflammation;  
KW macular degeneration; osteoporosis; Paget's disease;  
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX  
OS Mus sp.

XX  
XX WO9840488-A1.

XX  
XX 17-SEP-1998.

XX  
XX 12-MAR-1998; 98WO-US04987.

XX  
XX 12-MAR-1997; 97US-0039609.

XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX  
XX Johanson KO, Jonak ZL, Taylor AH;

XX  
XX WPI: 1999-034590/03.

XX  
XX N-PSDB; AAV71802.

XX  
XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
PT osteoporosis

XX  
PS Example 13; Page 64; 97pp; English.

XX  
XX This is the amino acid sequence of the region of the murine  
CC monoclonal antibody (MAB) D12 light chain variable region (VL)  
CC that is altered in humanised D12 VL (see also AAW84096). A  
CC synthetic gene (see AAV81902) encoding the protein was prepared  
CC from synthetic oligonucleotides and used to prepare an expression  
CC vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3  
CC vitronectin receptor MAB. Humanised D12 MABs can be used for  
CC passive immunotherapy of disorders mediated by the alpha-v beta-3  
CC vitronectin receptor, e.g. restenosis and angiogenic associated  
CC diseases.

XX

SQ Sequence 112 AA;

Query Match 90.9%; Score 510; DB 20; Length 112;  
Best Local Similarity 90.7%; Pred. No. 2.9e-32;  
Matches 97; Conservative 4; Mismatches 6; Indels

QY	1	EIVLTQSPATLSLSPGERATLSCAQSQSI	NHLHWYQORPGQAPRLLIKYRQSGT	SGTIPA	60
		:	:	:	
Db	1	divltspatlsispgeratlsr	asgsinhlhwqpgqaprllikyasqsg	ips	60
QY	61	RFSGSGSGYDFLTITSSLEPEDFAVY	YQQSGSWPHTFGGKTVEIK	107	
Db	61	rfsqsgsqtdfltsrlepedfavyv	qcsgnswpfficqatkv	ek	107

RESULT 10

AAW08946  
ID AAW08946 standard: Protein: 127 AA.

AA AAW08946:

XX  
DT 18-SEP-19XX  
XX  
DE  
XXXX Light chain revision[illegible]

KW human; epidermal growth factor; EGF; receptor; inhibition; growth;  
KW tumour; cell; late stage; prostatic; prostate; variable region.  
XX

XX  
XX

XX

XX

XXX

PR 07-JUN-1995; 95US-0482982.

PA (IMCL-) IMCLONE SYSTEMS INC.

XX  
FATBUDOCBEECS CWT (COWS)

[illegible]

DR N-PSDB: AAT49345.  
DR N-PSDB: AAT49345.

Chimeric and humanis

PT used for inhibiting tumour

Claim 31; Fig 19; 112pp; English.

of the reshaped human monoclonal

CC receptor.  
CC The MAb, or a fragment, can be used to inhibit the growth of tumour  
CC cells, especially late stage prostatic tumour cells in humans,  
CC optionally conjugated to a cytotoxic agent, especially doxorubicin,  
CC taxol or cisplatin, or a signal transduction, ras or cell cycle  
CC inhibitor.

Sequence 127 AA;

Query Match 90.4%; Score 507; DB 18; Length 127;  
Best Local Similarity 89.7%; Pred. No. 5.5e-32;  
Matches 96: Conservative 6: Mismatches 5: Indels

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYRSQISGIPA 60

SQ Sequence 107 AA;

Query Match 89.3%; Score 501; DB 18; Length 107;  
 Best Local Similarity 88.8%; Pred. NO. 1.3e-31;  
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIKYSQISGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIKYSQISGIPA 60

OY 61 RFSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107  
 DB 61 RFSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107

RESULT 12  
 AAW08949  
 ID AAW08949 standard; Protein; 107 AA.  
 XX  
 AC AAW08949;  
 XX  
 DT 18-SEP-1997 (first entry)  
 XX  
 DE Kappa light chain variable region of 225RB antibody.  
 XX  
 KW Kappa; light chain; reshaped; monoclonal; antibody; 225RB;  
 KW human; epidermal growth factor; EGF; receptor; inhibition; growth;  
 KW tumour; cell; late stage; prostatic; prostate; variable region;  
 KW framework; complementarity determining region; CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..23 /label= framework\_1  
 FT Region 24..34 /label= CDR\_1  
 FT Region 35..49 /label= framework\_2  
 FT Region 50..56 /label= CDR\_2  
 FT Region 57..88 /label= framework\_3  
 FT Region 89..97 /label= CDR\_3  
 FT Region 98..107 /label= framework\_4  
 XX  
 PN WO9640210-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96WO-US09847.  
 XX  
 PR 15-DEC-1995; 95US-0573289.  
 PR 07-JUN-1995; 95US-0482982.  
 XX  
 PA (IMCL-) INCLONE SYSTEMS INC.  
 PA (MRCC-) MRC COLLABORATIVE CENT.  
 XX  
 PI Giorgio NA, Goldstein NI, Jones ST, Saldanha JW;  
 XX WPI; 1997-051897/05.  
 DR  
 XX Chimeric and humanised versions of anti-EGF receptor antibody 225 -  
 PT used for inhibiting tumour growth, esp. of late stage prostatic  
 PT tumour  
 XX  
 PS Claim 29; Fig 21; 112pp; English.  
 XX  
 CC The present sequence is the kappa light chain variable region  
 CC of the reshaped human monoclonal antibody (MAB) H225, 225RKA. The

CC MAB is specific for the human epidermal growth factor (EGF)  
 CC receptor.  
 CC The MAB, or a fragment, can be used to inhibit the growth of tumour  
 CC cells, especially late stage prostatic tumour cells in humans,  
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,  
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle  
 CC inhibitor.  
 XX Sequence 107 AA;

Query Match 88.1%; Score 494; DB 18; Length 107;  
 Best Local Similarity 87.9%; Pred. NO. 4.6e-31;  
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIKYSQISGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGQAPRLLIKYSQISGIPA 60

OY 61 RFSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107  
 DB 61 RFSGSGTDFLTITSSLEPEDFAVYQCQSGSWPHTFGGKVEIK 107

RESULT 13  
 AAY32407  
 ID AAY32407 standard; Protein; 127 AA.  
 XX  
 AC AAY32407;  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Mouse anti-verotoxin II antibody VTml-1 humanised VL region.  
 XX  
 KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;  
 KW monoclonal antibody; light chain; mouse; humanised antibody; human;  
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
 XX HUS; therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..20 /note= "signal peptide"  
 FT Protein 21..127 /note= "mature protein"  
 FT Region 44..54 /note= "complementarity determining region 1"  
 FT Region 70..76 /note= "complementarity determining region 2"  
 FT Region 109..117 /note= "complementarity determining region 3"  
 XX  
 PN WO9959629-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 19-MAY-1999; 99WO-US11179.  
 XX  
 PR 20-MAY-1998; 98US-0086570.  
 XX  
 PA (TEIJ ) TEIJIN LTD.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;  
 XX WPI; 2000-086580/07.  
 DR N-PSDB; AAZ35244.  
 XX  
 PT Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli -

PS Claim 12; Fig 2b; 59pp; English.

XX This sequence represents a humanised light chain variable region of  
 CC murine monoclonal antibody Vm1-1 (MuVtm1-1), an antibody that  
 CC specifically binds to the B subunit of verotoxin II (VT2). The  
 CC invention relates to humanised antibodies against VT2 that are capable  
 CC of neutralising VT2 and/or VT2 variants. The humanised antibody is a  
 CC humanized form of MuVtm1-1 comprising the complementarity determining  
 CC regions of MuVtm1-1 and the heavy and light chain variable region  
 CC frameworks from the human GF4 antibody heavy and light chain  
 CC frameworks, provided that at least 1 position selected from L49, H29,  
 CC H30, H49 and H98 is occupied by the amino acid at the equivalent  
 CC position of the MuVtm1-1 antibody heavy or light chain variable region  
 CC framework. Such humanized antibodies have an affinity for VT2 that is  
 CC 3-, 5 or 10-times that of MuVtm1-1. They are used for treating a  
 CC patient suffering from, or at risk of, the toxic effects from VT2  
 CC (claimed), especially for treating verotoxin producing Escherichia  
 CC coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).

SQ Sequence 127 AA;

Query Match 87.3%; Score 490; DB 21; Length 127;

Best Local Similarity 89.7%; Pred. No. 1.1e-30; Mismatches 6; Indels 0; Gaps 0;  
 Matches 96; Conservative 5;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLTIKYRSQISGIPA 60  
 |||||  
 Db 21 eivltqspatlsvspgeratlsrasqtsinnhlhwyyqkpgqprlliksaqsigsipa 80  
 |||||

QY 61 RFGSGSGDTFTLTISLSEPEDFAVYVCQSGSWPHFTFGGKTVEIK 107  
 |||||

Db 81 rfgsgsgtdftltislesedfavyvcqsgswpftfgdggtkvek 127  
 |||||

RESULT 14

AAV30205  
 ID AAY30205 standard; Protein; 107 AA.

XX AAY30205;

DT 01-NOV-1999 (first entry)

DE The variable light chain of humanised antibody L3.17.

XX Light chain variable region; chimeric antibody; anti-CD40 antibody;  
 KW chi220; humoral immune response; T cell dependent antigen;  
 KW collagen induced arthritis; transplant induced rejection;  
 KW T cell mediated disorder; autoimmune disease; inflammatory disease;  
 KW transplantation.

XX Synthetic.

OS Homo sapiens.

XX WO942075-A2.

PN 26-AUG-1999.

XX 10-FEB-1999; 99WO-US02949.

XX 19-FEB-1998; 98US-0026291.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;  
 PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;

XX WPI; 1999-527408/44.

DR N-PSDB; AA210205.

XX Antibody that binds human CD40, for treating T cell mediated  
 PT disorders

XX

PS Claim 26; Page 33-34; 77pp; English.

XX The present sequence represents the variable light chain of humanised  
 CC antibody L3.17. The antibody is effective in modulating humoral immune  
 CC response against T cell dependent antigens, collagen induced arthritis  
 CC and transplant induced rejection. They are also useful for their  
 CC anti-inflammatory properties. The antibodies have wide therapeutic  
 CC applications, including autoimmune and inflammatory diseases and  
 CC transplantation. The antibody can be used in a pharmaceutical composition  
 CC for treating a patient suffering from a T cell mediated disorder. They  
 CC can also be used to treat autoimmune diseases, inflammatory diseases,  
 CC and transplantation.

XX Sequence 107 AA;

Query Match 87.2%; Score 489; DB 20; Length 107;

Best Local Similarity 88.8%; Pred. No. 1.1e-30; Mismatches 7; Indels 0; Gaps 0;  
 Matches 95; Conservative 5;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLTIKYRSQISGIPA 60  
 |||||

Db 1 eivltqspatlsvspgeratlsrasqtsidylhwyyqkpgqprlliyvashsigsipa 60  
 |||||

QY 61 RFGSGSGDTFTLTISLSEPEDFAVYVCQSGSWPHFTFGGKTVEIK 107  
 |||||

Db 61 rfgsgsgtdftltislespedfavyvcqsgswpftfgdggtkvek 107  
 |||||

RESULT 15

AAV30203

ID AAY30203 standard; Protein; 107 AA.

XX AAY30203;

DT 01-NOV-1999 (first entry)

DE The variable light chain of humanised antibody F4.

XX Light chain variable region; chimeric antibody; anti-CD40 antibody;  
 KW chi220; humoral immune response; T cell dependent antigen;  
 KW collagen induced arthritis; transplant induced rejection;  
 KW T cell mediated disorder; autoimmune disease; inflammatory disease;  
 KW transplantation.

XX Synthetic.

OS Homo sapiens.

XX WO942075-A2.

XX 26-AUG-1999.

XX 10-FEB-1999; 99WO-US02949.

XX 19-FEB-1998; 98US-0026291.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;  
 PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;

XX WPI; 1999-527408/44.

DR N-PSDB; AA210203.

XX Antibody that binds human CD40, for treating T cell mediated  
 PT disorders

XX Claim 21; Page 32-33; 77pp; English.

XX The present sequence represents the variable light chain of humanised  
 CC antibody F4. The antibody is effective in modulating humoral immune  
 CC response against T cell dependent antigens, collagen induced arthritis  
 CC and transplant induced rejection. They are also useful for their



CC anti-inflammatory properties. The antibodies have wide therapeutic  
CC applications, including autoimmune and inflammatory diseases and  
CC transplantation. The antibody can be used in a pharmaceutical composition  
CC for treating a patient suffering from a T cell mediated disorder. They  
CC can also be used to treat autoimmune diseases, inflammatory diseases,  
CC and transplantation.

XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 488; DB 20; Length 107;  
Best Local Similarity 88.8%; Pred. No. 1.3e-30;  
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGOAPRLIKYRSQISGIPA 60

DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGOAPRLIKYRSQISGIPA 60

QY 61 RFSGSGGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107

DB 61 RFSGSGGTDFLTITISLPEDFAVYYCQSGSWPHTFGGKVEIK 107

Search completed: October 11, 2001, 12:01:58  
Job time: 968 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:06 ; Search time 25.17 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-08-791-391A-4

Perfect score: 561  
Sequence: 1 E1VLTSPTATLSLSPGERAT.....COQSGSWPHFGGKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTOTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	91.3	107	US-07-634-278-63	Sequence 63, Appl
2	512	91.3	107	US-07-634-278-87	Sequence 87, Appl
3	512	91.3	107	US-08-477-728-63	Sequence 63, Appl
4	512	91.3	107	US-08-477-728-87	Sequence 87, Appl
5	512	91.3	107	US-08-474-040-63	Sequence 63, Appl
6	512	91.3	107	US-08-474-040-87	Sequence 87, Appl
7	512	91.3	107	US-08-487-200-63	Sequence 63, Appl
8	512	91.3	107	US-08-487-200-87	Sequence 87, Appl
9	512	91.3	107	US-08-484-537-63	Sequence 63, Appl
10	512	91.3	107	US-08-484-537-87	Sequence 87, Appl
11	486	86.6	127	US-08-476-176B-10	Sequence 10, Appl
12	486	86.6	127	US-08-127-721A-10	Sequence 10, Appl
13	486	86.6	127	US-08-485-246A-10	Sequence 10, Appl
14	480	85.6	127	US-08-476-176B-6	Sequence 6, Appl
15	480	85.6	127	US-08-127-721A-6	Sequence 6, Appl
16	480	85.6	127	US-08-485-246A-6	Sequence 6, Appl
17	479	85.4	107	US-08-232-081B-9	Sequence 9, Appl
18	477	85.0	127	US-08-476-176B-8	Sequence 8, Appl
19	477	85.0	127	US-08-127-721A-8	Sequence 8, Appl
20	477	85.0	127	US-08-485-246A-8	Sequence 8, Appl
21	448.5	79.9	107	US-08-783-853A-44	Sequence 44, Appl
22	447	79.7	107	US-07-634-278-62	Sequence 62, Appl
23	447	79.7	107	US-08-477-728-62	Sequence 62, Appl
24	447	79.7	107	US-08-474-040-62	Sequence 62, Appl
25	447	79.7	107	US-08-487-200-62	Sequence 62, Appl
26	447	79.7	107	US-08-484-537-62	Sequence 62, Appl
27	447	79.7	127	US-07-634-278-83	Sequence 83, Appl

28	447	79.7	127	1	US-08-477-728-83	Sequence 83, Appl
29	447	79.7	127	1	US-08-474-040-83	Sequence 83, Appl
30	447	79.7	127	1	US-08-487-200-83	Sequence 83, Appl
31	447	79.7	127	4	US-08-484-537-83	Sequence 83, Appl
32	444	79.1	127	1	US-08-436-463-4	Sequence 4, Appl
33	440	78.4	107	1	US-08-436-463-20	Sequence 20, Appl
34	440	78.4	109	1	US-07-942-245-4	Sequence 4, Appl
35	437	77.9	107	1	US-08-107-669D-1	Sequence 1, Appl
36	437	77.9	107	1	US-08-472-788A-1	Sequence 1, Appl
37	437	77.9	107	2	US-08-477-531B-1	Sequence 1, Appl
38	437	77.9	107	2	US-08-082-842A-1	Sequence 1, Appl
39	436	77.7	111	1	US-07-634-278-47	Sequence 47, Appl
40	436	77.7	111	1	US-08-477-728-47	Sequence 47, Appl
41	436	77.7	111	1	US-08-474-040-47	Sequence 47, Appl
42	436	77.7	111	1	US-08-487-200-47	Sequence 47, Appl
43	436	77.7	111	4	US-08-484-537-47	Sequence 47, Appl
44	431.5	76.9	107	3	US-08-783-853A-57	Sequence 57, Appl
45	429.5	76.6	108	2	US-08-232-081B-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1  
US-07-634-278-63  
; Sequence 63, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELLING, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single



Db 1 EIVLTQSPGTLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60  
QY 61 RFSGSGGTDFLTITSSLEPEDFAVYCYCOQSNWPHFTGGGKVEIK 107  
Db 61 RFSGSGGTDFLTITSSLEPEDFAVYCYCOQSNWPHFTGGGKVEIK 107

RESULT 4  
US-08-477-728-87  
; Sequence 87, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988

; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-477-728-87

Query Match 91.3%; Score 512; DB 1; Length 107;  
Best Local Similarity 91.6%; Pred. No. 5.6e-42;  
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYRQSISGIPA 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60  
QY 61 RFSGSGGTDFLTITSSLEPEDFAVYCYCOQSNWPHFTGGGKVEIK 107

Db 61 RFSGSGGTDFLTITSSLEPEDFAVYCYCOQSNWPHFTGGGKVEIK 107  
RESULT 5  
US-08-474-040-63  
; Sequence 63, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-474-040-63

Query Match 91.3%; Score 512; DB 1; Length 107;  
Best Local Similarity 91.6%; Pred. No. 5.6e-42;  
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYRQSISGIPA 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQISNNLHWYQKPGQAPRLLIKYASQISGIPD 60  
QY 61 RFSGSGGTDFLTITSSLEPEDFAVYCYCOQSNWPHFTGGGKVEIK 107  
Db 61 RFSGSGGTDFLTITSSLEPEDFAVYCYCOQSNWPHFTGGGKVEIK 107



APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-487-200-87

Query Match 91.3%; Score 512; DB 1; Length 107;  
Best Local Similarity 91.6%; Pred. No. 5.6e-42;  
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60  
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIKYSQISGIPD 60  
Qy 61 RFSGSGSGTDFLTITSLLEPEDFAVYYCQSGSWPHTFGGKTKVEIK 107  
Db 61 RFSGSGSGTDFLTITSLRLEPEDFAVYYCQGSNSWPHTFGGKTKVEIK 107

RESULT 9  
US-08-484-537-63  
; Sequence 63, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-537-63

Query Match 91.3%; Score 512; DB 4; Length 107;  
Best Local Similarity 91.6%; Pred. No. 5.6e-42;  
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60  
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQISNHLHWYQORPGQAPRLLIKYSQISGIPD 60  
Qy 61 RFSGSGSGTDFLTITSLLEPEDFAVYYCQSGSWPHTFGGKTKVEIK 107  
Db 61 RFSGSGSGTDFLTITSLRLEPEDFAVYYCQGSNSWPHTFGGKTKVEIK 107

RESULT 10  
US-08-484-537-87  
; Sequence 87, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.





; FILING DATE: 27-SEPTEMBER-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6066718ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-127-721A-10

Query Match 85.6%; Score 486; DB 3; Length 127;  
Best Local Similarity 86.0%; Pred. No. 2e-39; Mismatches 8; Indels 0; Gaps 0;  
Matches 92; Conservative 7;  
QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIKYSQISGIPA 60  
DB 21 EIVLTQSPGTLSPGERATLSCRASQISGNIHWYQKPGQAPRLLIKAYESISGIPS 80  
QY 61 RFSGSGGTDFLTITSLLEPEDFAVYCYQSQSWPHTFGGKVEIK 107  
DB 81 RFSGSGGTDFLTITSLRLEPEDFAMVYCYQSDSWPTTFGGTKVEIK 127

RESULT 13  
US-08-485-246A-10  
; Sequence 10, Application US/08485246A  
; Patent No. 6072035  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 6072035man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Reshaped monoclonal isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6072035artis Patent Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,246A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/127,721  
; FILING DATE: 27-SEPTEMBER-1993  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6072035ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-246A-10

Query Match 86.6%; Score 486; DB 3; Length 127;  
Best Local Similarity 86.0%; Pred. No. 2e-39; Mismatches 8; Indels 0; Gaps 0;  
Matches 92; Conservative 7;  
QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIKYSQISGIPA 60  
DB 21 EIVLTQSPGTLSPGERATLSCRASQISGNIHWYQKPGQAPRLLIKAYESISGIPS 80  
QY 61 RFSGSGGTDFLTITSLLEPEDFAVYCYQSQSWPHTFGGKVEIK 107  
DB 81 RFSGSGGTDFLTITSLRLEPEDFAMVYCYQSDSWPTTFGGTKVEIK 127

RESULT 14  
US-08-476-176B-6  
; Sequence 6, Application US/08476176B  
; Patent No. 5958708  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 5958708man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Immunoglobulin isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5958708artis Patent Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,176B  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/127,721  
; FILING DATE: 27-SEPTEMBER-1993  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5958708ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-476-176B-6

Query Match 85.6%; Score 480; DB 2; Length 127;  
Best Local Similarity 84.1%; Pred. No. 7.4e-39;  
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 21 DILLTQSPGTLSPGERATLSCRASQISGNTNIHWYQKPGQAPRLLIKYSSESIGIPS 80  
QY 61 RFSGSGSGTDFLTITISLEPEDFAVYCCQSGSWPHTFGGKVEIK 107  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 81 RFSGSGSGTDFLTITISLEPEDFAVYCCQSGSDSWPTTFGGKVEIK 127

## RESULT 15

US-08-127-721A-6  
; Sequence 6, Application US/08127721A  
; Patent No. 6066718  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 6066718man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Immunoglobulin isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6066718artis Patent and Trademark Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,721A  
; FILING DATE: 27-SEPTEMBER-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6066718ak, Henry P.  
; REGISTRATION NUMBER: 33,200  
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-127-721A-6

Query Match 85.6%; Score 480; DB 3; Length 127;  
Best Local Similarity 84.1%; Pred. No. 7.4e-39;  
Matches 90; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIKYSQISGIPA 60  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 21 DILLTQSPGTLSPGERATLSCRASQISGNTNIHWYQKPGQAPRLLIKYSSESIGIPS 80  
QY 61 RFSGSGSGTDFLTITISLEPEDFAVYCCQSGSWPHTFGGKVEIK 107  
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
Db 81 RFSGSGSGTDFLTITISLEPEDFAVYCCQSGSDSWPTTFGGKVEIK 127

Search completed: October 11, 2001, 12:01:06  
Job time: 916 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:31 ; Search time 2122.65 Seconds  
(without alignments)  
2557.737 Million cell updates/sec

Title: US-08-791-391A-5  
Perfect score: 351  
Sequence: 1 GAAGGCACGCTGGTGAGTC.....CTCTGGTCACGTCTCTGTGCA 351

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_bal:\*
- 2: gb\_bal2:\*
- 3: gb\_bal3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_om:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_pl1:\*
- 13: gb\_pl2:\*
- 14: gb\_pl3:\*
- 15: gb\_pl4:\*
- 16: em\_bal:\*
- 17: em\_bal2:\*
- 18: em\_fun:\*
- 19: em\_htgo\_hum:\*
- 20: em\_htgo\_inv:\*
- 21: em\_htgo\_rod:\*
- 22: em\_htg\_hum1:\*
- 23: em\_htg\_hum2:\*
- 24: em\_htg\_hum3:\*
- 25: em\_htg\_hum4:\*
- 26: em\_htg\_hum5:\*
- 27: em\_htg\_hum6:\*
- 28: em\_htg\_hum7:\*
- 29: em\_htg\_hum8:\*
- 30: em\_htg\_inv1:\*
- 31: em\_htg\_inv2:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_rod:\*
- 34: em\_hum1:\*
- 35: em\_hum2:\*
- 36: em\_hum3:\*
- 37: em\_hum4:\*
- 38: em\_hum5:\*
- 39: em\_hum6:\*
- 40: em\_hum7:\*
- 41: em\_in:\*
- 42: em\_om:\*
- 43: em\_or:\*

- 44: em\_ov:\*
- 45: em\_pat:\*
- 46: em\_ph:\*
- 47: em\_pl:\*
- 48: em\_rod:\*
- 49: em\_sts:\*
- 50: em\_sy:\*
- 51: em\_un:\*
- 52: em\_v1:\*
- 53: gb\_sts1:\*
- 54: gb\_sts2:\*
- 55: gb\_sts3:\*
- 56: gb\_sy:\*
- 57: gb\_un:\*
- 58: gb\_v1:\*
- 59: gb\_v2:\*
- 60: gb\_htg1:\*
- 61: gb\_htg2:\*
- 62: gb\_htg3:\*
- 63: gb\_htg4:\*
- 64: gb\_htg5:\*
- 65: gb\_htg6:\*
- 66: gb\_htg7:\*
- 67: gb\_htg8:\*
- 68: gb\_htg9:\*
- 69: gb\_htg10:\*
- 70: gb\_htg11:\*
- 71: gb\_htg12:\*
- 72: gb\_htg13:\*
- 73: gb\_htg14:\*
- 74: gb\_htg15:\*
- 75: gb\_htg16:\*
- 76: gb\_htg17:\*
- 77: gb\_htg18:\*
- 78: gb\_htg19:\*
- 79: gb\_htg20:\*
- 80: gb\_htg21:\*
- 81: gb\_htg22:\*
- 82: gb\_htg23:\*
- 83: gb\_htg24:\*
- 84: gb\_htg25:\*
- 85: gb\_pr1:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_rod1:\*
- 95: gb\_rod2:\*
- 96: gb\_rod3:\*
- 97: gb\_rod4:\*
- 98: em\_bal3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	351	100.0	351	9 AX060784	AX060784 Sequence
2	309.4	88.1	482	10 I08289	I08289 Sequence 6
3	309.4	88.1	488	95 S45356	S45356 immunoglobu
4	302.2	86.1	351	9 AX060780	AX060780 Sequence
5	296.6	84.5	413	9 A38870	A38870 Sequence 24
6	295	84.0	413	9 AR013776	AR013776 Sequence
7	294.8	84.0	354	94 MUSIGMUD2A	M83724 Mouse monoc
8	293.6	83.6	721	9 AR027762	AR027762 Sequence



```
Qy 241 CTGCAATGAGCAGTCTGAATCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 372 CTGCAATGAGCAGTCTGAATCTCTGAGGACACAGCCGTGTATTACTGTGCAAGAGGTAC 431
Qy 301 TACGCCAGTTTGTCTACTTGGGGCAAGGACTCTGGTCACTGCTCTGCA 351
Db 432 GGCCTCCCTTTTGTCTACTTGGGGCAAGGACTCTGGTCACTGCTCTGCA 482

RESULT 3
LOCUS S45356 488 bp mRNA ROD 08-MAY-1993
DEFINITION immunoglobulin heavy chain variable-anti-human IL-2R [mice, mRNA
ACCESSION S45356
VERSION S45356
KEYWORDS S45356.1 GI:255660
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 488)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Rose,B., Gillespie,A., Wunderlich,D., Kelley,K., Dzuiba,J.,
Shedd,D., Cahill,K. and Zerler,B.
JOURNAL Differential effects of a murine and chimeric mouse/human
MEDLINE anti-interleukin-2 receptor antibody on human T-cell proliferation
REMARK Immunology 76 (3), 452-459 (1992)
92406249
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 115041] from the original journal article.
This sequence comes from Fig. 1b.
FEATURES
source
1..488
/organism="Mus sp."
/db_xref="taxon:10095"
gene
80..487
/partial
/gene="immunoglobulin heavy chain variable"
CDS
80..487
/partial
/gene="immunoglobulin heavy chain variable"
/gene="immunoglobulin heavy chain variable"
/note="anti-human IL-2R; This sequence comes from Fig. 1b"
/codon_start=1
/product="immunoglobulin heavy chain variable"
/protein_id="AAB23305.1"
/db_xref="GI:255661"
/translation="MNPGLRLFLVLTKGVKEVQLVESGGGLVKPGSKLSKLAAS
GFAPSSIDMSVWROTPEKRLWYVAYISSGDNTYPTVKGRTFISRDNAKNTLYLQM
SSLKSEDTAVYYCARYGGLPFAYWGQGLTVTSA"
BASE COUNT 114 a 116 c 132 g 126 t
ORIGIN

Query Match 88.1%; Score 309.4; DB 95; Length 488;
Best Local Similarity 92.6%; Pred. No. 4e-95;
Matches 325; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 GAAGTGACGCTGTGGAGCTCTGGGGAGCGTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60
Db 137 GAAGTGACGCTGTGGAGCTCTGGGGAGCGTTAGTGAAGCCTGGAAGTCCCTGAAACTC 196
Qy 61 TCCTGTGAGCCTCTGGATTGCTTTCAGTAGCATATGACATGCTCTTGGGTTTCGCCAGATT 120
Db 197 TCCTGTGAGCCTCTGGATTGCTTTCAGTAGCATATGACATGCTCTTGGGTTTCGCCAGACT 256
Qy 121 CCGGAGAGAGCGCTGGAGTGGTGCAGAAAGTTAGTAGTGTGGTGGTAGCACCTACTAT 180
Db 257 CCGGAGAGAGCGCTGGAGTGGTGCATACATTTAGTAGTGTGGTGGTAGAACCTACTAT 316
Qy 181 TTAGACACTGTGAGGCGCGATTCACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 240
Db 317 CCAGACACTGTGAGGCGCGATTCACCATCTCCAGAGACAATGCCAAGACACCCCTTTAC 376
```

```
Qy 241 CTGCAATGAGCAGTCTGAATCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 377 CTGCAATGAGCAGTCTGAAGTCTCTGAGGACACAGCCGTGTATTACTGTGCAAGAGGTAC 436
Qy 301 TACGCCAGTTTGTCTACTTGGGGCAAGGACTCTGGTCACTGCTCTGCA 351
Db 437 GGCCTCCCTTTTGTCTACTTGGGGCAAGGACTCTGGTCACTGCTCTGCA 487

RESULT 4
LOCUS AX060780 351 bp DNA PAT 22-JAN-2001
DEFINITION Sequence 1 from Patent WO0078815.
ACCESSION AX060780
VERSION AX060780.1 GI:12406160
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 351)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 1 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1..351
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>351
/note="grafted antibody variable region"
/codon_start=1
/translation="QVQLVSGGVSVPQGRSLRSLSCAASGFTFSSYDMSVWROAPGKG
LEWVAKYSSGGSGTYLDVQGRFTISRDNKNTLYLQMNSLRADTAVYYCARHNTY
SFAYWGQGLTVTSS"
BASE COUNT 80 a 82 c 104 g 85 t
ORIGIN

Query Match 86.1%; Score 302.2; DB 9; Length 351;
Best Local Similarity 91.9%; Pred. No. 1.1e-92;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 2 AAGTGACGCTGTGGAGTCTGGGGAGCGTTAGTGAAGCCTGGAAGTCCCTGAGACTCT 61
Db 2 AAGTGACGCTGTGGAGTCTGGGGAGCGTTGTGCAGCCTGGAAGTCCCTGAGACTCT 61
Qy 62 CCTGTGACGCTCTGGATTGCTTTCAGTAGCATATGACATGCTTGGGTTGCCAGATTTC 121
Db 62 CCTGTGACGCTCTGGATTGCTTTCAGTAGCATATGACATGCTTGGGTTGCCAGGCTC 121
Qy 122 CGGGAAGAGCGCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTATT 181
Db 122 CGGGAAGAGCGCTGGAGTGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTATT 181
Qy 182 TAGACACTGTGAGGCGCGATTTCACCATCTCCAGAGACAATGCCAAGACACCCCTATACC 241
Db 182 TAGACACTGTGAGGCGCGATTTCACCATCTCCAGAGACAATGCCAAGACACCCCTATACC 241
Qy 242 TGCAATCAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAACT 301
Db 242 TGCAATCAGCAGTCTGAGAGCGCGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT 301
Qy 302 ACGGCAAGTTTGTCTTACTTGGGGCCCAAGGACTCTGGTCACTGCTCTCT 348
Db 302 ACGGCAAGTTTGTCTTACTTGGGGCCCAAGGACTCTACAGTCACTGCTCTCT 348

RESULT 5
A38870
```

```
LOCUS       A38870               413 bp    DNA                    PAT      05-MAR-1997
DEFINITION   Sequence 24 from Patent WO9413805.
ACCESSION    A38870
VERSION      A38870.1  GI:2295288
KEYWORDS     unclassified.
SOURCE       unclassified.
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 413)
AUTHORS      King,D.J., Adair,J.R. and Owens,R.J.
TITLE        HUMANISED ANTIBODIES DIRECTED AGAINST A33 ANTIGEN
JOURNAL      Patent: WO 9413805-A 24 23-JUN-1994;
              CELTECH LTD (GB)
COMMENT      Other publication GB 5656894 940704
              Other publication GB 2278357 941130
              Other publication JP 7504334T 950518.
FEATURES     Location/Qualifiers
             source
             1..413
             /organism="unidentified"
             /db_xref="taxon:32644"
BASE COUNT   88 a  99 c 118 g 108 t
ORIGIN
Query Match      84.5%; Score 296.6; DB 9; Length 413;
Best Local Similarity 90.3%; Pred. No. 9.7e-91;
Matches 317; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 GAAGTCACGCTGTGGAGCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTCGACACTC 60
Db 63 GAAGTGAAGCTGTGGAGCTGGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTCGAAACTC 122
QY 61 TCCTGTGACAGCTCTGAGTTCGCTTTCAGTAGCTATGACATGCTTTCAGTTCGCGAGAT 120
Db 123 TCCTGTGACAGCTCTGAGTTCGCTTTCAGTAGCTATGACATGCTTTCAGTTCGCGAGAT 182
QY 121 CCGGAGAAGAGGCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTGGTAGCAGCTACTAT 180
Db 183 CCGGAGAAGAGGCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTGGTAGCAGCTACTAT 242
QY 181 TTAGACACTGTGACAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
Db 243 TTAGACAGTGTGAAGGCGGATTCACCATCTCCAGAGACAGTCCCAGAACACCCCTATAC 302
QY 241 CTGCAATGAGCAGCTCTGAACTCTGAGGACACAGCCATGTTACTGTGCAAGACATAAC 300
Db 303 CTGCAATGAGCAGCTCTGAGGCTGAGGACACAGCCCTTGTATTACTGTGACCGACTAGC 362
QY 301 TAGCGCAGTTTTCCTTACTGGGGCCCAAGGACTCTGCTCACTGCTCTGCA 351
Db 363 GTAGTCCCGTTTGCCTTACTGGGGCCCAAGGACTCTGCTCACTGCTCTGCA 413

RESULT      7
MUSIGMUD2A  354 bp    mRNA                    ROD      08-MAY-2000
LOCUS       MUSIGMUD2A  354 bp    mRNA                    ROD      08-MAY-2000
DEFINITION   Mouse monoclonal antiidiotypic antibody IgM VDJ-region mRNA.
ACCESSION    M83724
VERSION      M83724.1  GI:197951
KEYWORDS     D-region; Ig heavy chain; J-region; V-region; immunoglobulin;
              immunoglobulin mu-chain; monoclonal antiidiotypic antibody.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 354)
AUTHORS      Taub,R., Hsu,J.C., Garsky,V.M., Hill,B.L., Erlanger,B.F. and
              Kohn,L.D.
TITLE        Peptide sequences from the hypervariable regions of two monoclonal
              anti-idiotypic antibodies against the thyrotropin (TSH) receptor
              are similar to TSH and inhibit TSH-increased cAMP production in
              FRTL-5 thyroid cells
JOURNAL      J. Biol. Chem. 267 (9), 5977-5984 (1992)
MEDLINE      92210565
FEATURES     Location/Qualifiers
             source
             1..354
             /organism="Mus musculus"
             /db_xref="taxon:10090"
             /map="chromosome 6"
             /cell_line="4G11"
             /tissue_type="hybridoma"
             <1..>354
             /gene="IgM"
             <1..>354
             /codon_start=1
             /product="immunoglobulin mu chain"
             /protein_id="AA53040.1"
             /db_xref="GI:197952"
             /translation="EVOLVEGGGLVKPGSLKLSAASGTFSSYAMSWVRSPEKR
              LEWVAEISSGGSYTYPTVTGRFTISRDNKNTLYLEMSRSDTAMYYCARDGYY
              VRFAYWGQGLTVTSA"
             <1..>294
             /gene="IgM"
V_region
```

```
D_segment      295..309
J_segment      310..>354
BASE COUNT    79 a      81 c      108 g      86 t
ORIGIN
Query Match      84.0%; Score 294.8; DB 94; Length 354;
Best Local Similarity 91.5%; Pred. No. 4e-90; 27; Indels 3; Gaps 1;
Matches 324; Conservative 0; Mismatches 0;

Qy 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAGACTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAAACTC 60

Qy 61 TCCTGTGAGCCTCTGGATTCCTTTCAAGTAGTATGACATGCTTTGGTTCGCCAGATT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCCTGTGAGCCTCTGGATTCCTTTCAAGTAGTATGACATGCTTTGGTTCGCCAGATT 120

Qy 121 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTACCTACTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTACCTACTAT 180

Qy 181 TTAGACACTGTGACGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CCAGACACTGTGACGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTGTAC 240

Qy 241 CTGCAATGACAGCTCTGAACCTCTGAGACACAGCCATGTATTACTGTGCAAGACA---T 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CTGCAATGACAGCTCTGAACCTCTGAGACACAGCCATGTATTACTGTGCAAGGATGGT 300

Qy 298 AACTACGGCAGTTTTCCTTACTTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TACTACGTGAGTTGCTTACTTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 354

RESULT 8
AR027762
LOCUS      AR027762      721 bp      DNA      PAT      29-SEP-1999
DEFINITION Sequence 15 from patent US 5856456.
ACCESSION AR027762
VERSION   AR027762.1 GI:5938582
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 721)
AUTHORS  Whitlow,M.D. and Filpula,D.R.
TITLE    Linker for linked fusion polypeptides
JOURNAL  Patent: US 5856456-A 15 05-JAN-1999;
FEATURES
          Location/Qualifiers
            source
              1..721
                /organism="unknown"
BASE COUNT 176 a      172 c      189 g      184 t
ORIGIN

Query Match      83.6%; Score 293.6; DB 9; Length 721;
Best Local Similarity 90.2%; Pred. No. 1.1e-89;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAGACTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 364 GAAATGAAAGCTTGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAAACTC 423

Qy 61 TCCTGTGAGCCTCTGGATTCCTTTCAAGTAGTATGACATGCTTTGGTTCGCCAGATT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 424 TCCTGTGAGCCTCTGGATTCCTTTCAAGTAGTATGACATGCTTTGGTTCGCCAGACT 483

Qy 121 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTAGCAGCTACTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 484 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTAGCAGCTACTAT 543

Qy 181 TTAGACACTGTGACGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 544 TTAGACACTGTGAGGGCCGATTCACCATCTCCAGAGAGTGGCCAGAACACCCCTATAC 603

Qy 241 CTGCAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 604 CTGCAATGACAGCTCTGAGGCTCTGAGGACACAGCCCTTGTATTACTGTGACCGACTACG 663

Qy 301 TAGGCACTTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 GTAGTCCGCGTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCT 711

RESULT 10
AR027763
LOCUS      AR027763      733 bp      DNA      PAT      29-SEP-1999
DEFINITION Sequence 17 from patent US 5856456.
ACCESSION AR027763
VERSION   AR027763.1 GI:5938583
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
```

```
D_segment      295..309
J_segment      310..>354
BASE COUNT    79 a      81 c      108 g      86 t
ORIGIN
Query Match      84.0%; Score 294.8; DB 94; Length 354;
Best Local Similarity 91.5%; Pred. No. 4e-90; 27; Indels 3; Gaps 1;
Matches 324; Conservative 0; Mismatches 0;

Qy 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAGACTC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 544 TTAGACACTGTGAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 603

Qy 241 CTGCAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 604 CTGCAATGACAGCTCTGAGGCTCTGAGGACACAGCCCTTGTATTACTGTGACCGACTACG 663

Qy 301 TAGGCACTTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 GTAGTCCGCGTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCT 711

RESULT 9
AR088763
LOCUS      AR088763      721 bp      DNA      PAT      07-SEP-2000
DEFINITION Sequence 15 from patent US 5990275.
ACCESSION AR088763
VERSION   AR088763.1 GI:10015526
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 721)
AUTHORS  Whitlow,M.D. and Filpula,D.R.
TITLE    Linker and linked fusion polypeptides
JOURNAL  Patent: US 5990275-A 15 23-NOV-1999;
FEATURES
          Location/Qualifiers
            source
              1..721
                /organism="unknown"
BASE COUNT 176 a      172 c      189 g      184 t
ORIGIN

Query Match      83.6%; Score 293.6; DB 9; Length 721;
Best Local Similarity 90.2%; Pred. No. 1.1e-89;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GAAATGACAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAGACTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 364 GAAATGAAAGCTTGTGGAGTCTGGGGAGGCTTAGTGAAGCTTGAAGCTGCCCTGAAACTC 423

Qy 61 TCCTGTGAGCCTCTGGATTCCTTTCAAGTAGTATGACATGCTTTGGTTCGCCAGATT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 424 TCCTGTGAGCCTCTGGATTCCTTTCAAGTAGTATGACATGCTTTGGTTCGCCAGACT 483

Qy 121 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTAGCAGCTACTAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 484 CCGGAGAGAGGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTAGCAGCTACTAT 543

Qy 181 TTAGACACTGTGACGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 544 TTAGACACTGTGAGGGCCGATTCACCATCTCCAGAGAGTGGCCAGAACACCCCTATAC 603

Qy 241 CTGCAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 604 CTGCAATGACAGCTCTGAGGCTCTGAGGACACAGCCCTTGTATTACTGTGACCGACTACG 663

Qy 301 TAGGCACTTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 GTAGTCCGCGTTTGTCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCT 711

RESULT 10
AR027763
LOCUS      AR027763      733 bp      DNA      PAT      29-SEP-1999
DEFINITION Sequence 17 from patent US 5856456.
ACCESSION AR027763
VERSION   AR027763.1 GI:5938583
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
```





```
Db 61 TCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATACCATGCTCTTGGTTGCCAGACT 120
QY 121 CCGGAGAAGAGGCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
Db 121 CCGGAGAAGAGGCTGGAGTGGGTGCGAACCATTAGTAGTGGTGGTTAAACACCTACTAT 180
QY 181 TTAGACACTGTGCAGGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
Db 181 CCAGACAGTGTGAAGGGTCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 240
QY 241 CTGCAAAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 241 CTGCAAAATGACAGCTCTGAGGCTCTGAGGACACAGCCCTGTATTACTGTGCAAGAGGTTAC 300
QY 301 TACGG---CAGTTTTCCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 351
Db 301 TATAGTAACCTACTTTGCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 354

RESULT 13
AF113107 354 bp mRNA ROD 21-SEP-2000
LOCUS Mus musculus hybridoma Y6-8G3 anti-myeloperoxidase immunoglobulin
DEFINITION heavy chain variable region mRNA, partial cds.
ACCESSION AF113107
VERSION AF113107.1 GI:4768654
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Jethwa, H.S., Clarke, S.H., Itoh-Lindstrom, Y., Falk, R.J.,
Jennette, J.C. and Nachman, P.H.
TITLE Restriction in Vkappa gene use and antigen selection in
anti-myeloperoxidase response in mice
JOURNAL J. Immunol. 165 (7), 3890-3897 (2000)
MEDLINE 20487209
REFERENCE 2 (bases 1 to 354)
AUTHORS Jethwa, H.S., Nachman, P.H., Jennette, J.C., Falk, R.J., Kinjoh, K.,
Tuttle, R. and Taylor, J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
FEATURES
source
1..354
/organism="Mus musculus"
/strain="SCG/Kj"
/db_xref="taxon:10090"
/cell_line="hybridoma Y6-8G3"
<1..>354
/feature="VH 7183; anti-MPO"
/codon_start=1
/product="anti-myeloperoxidase immunoglobulin heavy chain
variable region"
/protein_id="AAD29597.1"
/db_xref="GI:4768655"
/translation="EVMLVESGGGLVKPGSLKLSCAASGFTFSSTMSWVROTPEKR
LEWATISSGGNTYYPDSVKGRFTISRDNKNLXLQMSLSRSEDIALYICARGYYS
NYFAYWGQGLTVTSA"
BASE COUNT 84 a 80 c 102 g 88 t
ORIGIN

Query Match 82.6%; Score 290; DB 94; Length 354;
Best Local Similarity 90.7%; Pred. No. 1.8e-88;
Matches 321; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCTGAGACTC 60
Db 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCTGAGACTC 60
QY 61 TCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATACCATGCTCTTGGTTGCCAGACT 120
```

```
Db 61 TCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATACCATGCTCTTGGTTGCCAGACT 120
QY 121 CCGGAGAAGAGGCTGGAGTGGGTGCGAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
Db 121 CCGGAGAAGAGGCTGGAGTGGGTGCGAACCATTAGTAGTGGTGGTTAAACACCTACTAT 180
QY 181 TTAGACACTGTGCAGGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
Db 181 CCAGACAGTGTGAAGGGTCGATTCACCATCTCCAGAGACAATGCCAAGAACACCTGTAC 240
QY 241 CTGCAAAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 241 CTGCAAAATGACAGCTCTGAGGCTCTGAGGACACAGCCCTGTATTACTGTGCAAGAGGTTAC 300
QY 301 TACGG---CAGTTTTCCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 351
Db 301 TATAGTAACCTACTTTGCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 354

RESULT 14
AF113108 354 bp mRNA ROD 21-SEP-2000
LOCUS Mus musculus hybridoma Y6-9G3 anti-myeloperoxidase immunoglobulin
DEFINITION heavy chain variable region mRNA, partial cds.
ACCESSION AF113108
VERSION AF113108.1 GI:4768656
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Jethwa, H.S., Clarke, S.H., Itoh-Lindstrom, Y., Falk, R.J.,
Jennette, J.C. and Nachman, P.H.
TITLE Restriction in Vkappa gene use and antigen selection in
anti-myeloperoxidase response in mice
JOURNAL J. Immunol. 165 (7), 3890-3897 (2000)
MEDLINE 20487209
REFERENCE 2 (bases 1 to 354)
AUTHORS Jethwa, H.S., Nachman, P.H., Jennette, J.C., Falk, R.J., Kinjoh, K.,
Tuttle, R. and Taylor, J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
FEATURES
source
1..354
/organism="Mus musculus"
/strain="SCG/Kj"
/db_xref="taxon:10090"
/cell_line="hybridoma Y6-9G3"
<1..>354
/feature="VH 7183; anti-MPO"
/codon_start=1
/product="anti-myeloperoxidase immunoglobulin heavy chain
variable region"
/protein_id="AAD29598.1"
/db_xref="GI:4768657"
/translation="EVMLVESGGGLVKPGSLKLSCAASGFTFSSTMSWVROTPEKR
LEWATISSGGNTYYPDSVKGRFTISRDNKNLXLQMSLSRSEDIALYICARGYYS
NYFAYWGQGLTVTSA"
BASE COUNT 84 a 80 c 102 g 88 t
ORIGIN

Query Match 82.6%; Score 290; DB 94; Length 354;
Best Local Similarity 90.7%; Pred. No. 1.8e-88;
Matches 321; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCTGAGACTC 60
Db 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCTGAGACTC 60
```

```
QY 61 TCCTGTGACGCTCTGATTGCGTTTCAGTAGTATGACATGCTTTGGGTTCCGCAGATT 120
    |||
Db 61 TCCTGTGACGCTCTGATTGCGTTTCAGTAGTATGACATGCTTTGGGTTCCGCAGATT 120
    |||
QY 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTAT 180
    |||
Db 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTAT 180
    |||
QY 181 TTAGACACTGTGACAGGCCCATTCACCATCTCCAGAGACAAATCCCAAGACACCCCTATAC 240
    |||
Db 181 CCAGACAGTGTGAAGGCTGATTCACCATCTCCAGAGACAAATCCCAAGACACCCCTATAC 240
    |||
QY 241 CTGCAATGACAGCTGTGAGGCTGTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
    |||
Db 241 CTGCAATGACAGCTGTGAGGCTGTGAGGACACAGCCATGTATTACTGTGCAAGAGTTAC 300
    |||
QY 301 TACGG---CAGTTTGTCTTACTGGGGCCAAAGGACACTGTGCTACTGTCTCTGCA 351
    |||
Db 301 TATAGTAACACTACTTTGCTTACTGGGGCCAAAGGACACTGTGCTACTGTCTCTGCA 354
    |||

RESULT 15
MUSIGHNRZ
LOCUS MUSIGHNRZ 350 bp mRNA ROD 23-SEP-1994
DEFINITION Mus musculus Igh chain A allele of At8-1-12 mRNA, VDJ region.
ACCESSION M28187
VERSION M28187.1 GI:548170
KEYWORDS D-segment; J-segment; V-region; V-segment; immunoglobulin;
immunoglobulin heavy chain.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) newborn cdna
to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 350)
AUTHORS Komori,T., Sugiyama,H. and Kishimoto,S.
TITLE A novel V-H-DJ-H to J-H joining that induces H chain production in
an Ig-null immature B cell line
JOURNAL J. Immunol. 143, 1040-1045 (1989)
MEDLINE 89309739
COMMENT On Sep 24, 1994 this sequence version replaced gi:341843.
FEATURES
    Location/Qualifiers
        1..350
            /organism="Mus musculus"
            /strain="BALB/c"
            /sub_species="domesticus"
            /db_xref="taxon:10090"
            /cell_line="MuLV-transformed cell line At8-1"
            /dev_stage="newborn"
            /map="12"
            1..350
            /gene="Igh"
            <1..293
            /gene="Igh"
            <1..>293
            /gene="Igh"
            /note="this CDS feature is included to show the
            translation of the corresponding V-segment. Presently
            translation qualifiers on V-segment features are illegal."
            /codon_start=1
            /protein_id="AAA38413.1"
            /db_xref="GI:548171"
            /translation="EVMVLVSGGLVKPGSLKLSCAAAGTFFSSYAMSWVRQTPKRR
            LEWVATISSGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYICA"
            <1..>350
            /gene="Igh"
            /codon_start=1
            /product="immunoglobulin heavy chain"
            /protein_id="AAA38414.1"
            /db_xref="GI:548172"
            /translation="EVMVLVSGGLVKPGSLKLSCAAAGTFFSSYAMSWVRQTPKRR
            LEWVATISSGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYICASNVTPL
            GLTCAKGLWSLSL"
```

```
D_segment 294..302
J_segment /gene="Igh"
303..>350
BASE COUNT 78 a 81 c 105 g 86 t
ORIGIN
Query Match 82.5%; Score 289.4; DB 94; Length 350;
Best Local Similarity 90.9%; Pred. No. 2.8e-88;
Matches 319; Conservative 0; Mismatches 31; Indels 1; Gaps 1;
QY 1 GAAGTGCAGCTGGTGGAGCTTGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTCGAGACTC 60
    |||
Db 1 GAAGTGCAGCTGGTGGAGCTTGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTCGAGACTC 60
    |||
QY 61 TCCTGTGACGCTCTGATTGCGTTTCAGTAGTATGACATGCTTTGGGTTCCGCAGATT 120
    |||
Db 61 TCCTGTGACGCTCTGATTGCGTTTCAGTAGTATGACATGCTTTGGGTTCCGCAGACT 120
    |||
QY 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTAT 180
    |||
Db 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTAT 180
    |||
QY 181 TTAGACACTGTGACAGGCCCATTCACCATCTCCAGAGACAAATCCCAAGACACCCCTATAC 240
    |||
Db 181 CCAGACAGTGTGAAGGCTGATTCACCATCTCCAGAGACAAATCCCAAGACACCCCTATAC 240
    |||
QY 241 CTGCAATGACAGCTGTGAGGCTGTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
    |||
Db 241 CTGCAATGACAGCTGTGAGGCTGTGAGGACACAGCCATGTATTACTGTGCAAG-TATGGT 299
    |||
QY 301 TACGGCAGTTTTCTTACTGGGGCCAAAGGACACTGTGCTACTGTCTCTGCA 351
    |||
Db 300 AACTCCTGGTTTCTTACTGGGGCCAAAGGACACTGTGCTACTGTCTCTGCA 350
    |||
```

Search completed: October 11, 2001, 15:09:32  
Job time: 6354 sec

---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on:           October 11, 2001, 14:34:02 ; Search time 2341.88 Seconds  
                  (without alignments)  
                  1416.790 Million cell updates/sec

Title:            US-08-791-391A-5  
Perfect score:    351  
Sequence:        1 GAAGTCACGCTGGTGGAGTC.....CTCTGCTCAGTGTCTCTGCA 351

Scoring table:   IDENTITY NUC  
                  Gapop 10.0 , Gapext 1.0

Searched:       10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters:   20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
                  Maximum Match 100%  
                  Listing first 45 summaries

Database :       EST:\*

1:	gb_estl1:*	44:	em_esthum10:*
2:	gb_est2:*	45:	em_esthum11:*
3:	gb_est3:*	46:	em_esthum12:*
4:	gb_est4:*	47:	em_esthum13:*
5:	gb_est5:*	48:	em_esthum14:*
6:	gb_est6:*	49:	em_esthum15:*
7:	gb_est7:*	50:	em_esthum16:*
8:	gb_est8:*	51:	em_esthum17:*
9:	gb_est9:*	52:	em_esthum18:*
10:	gb_est10:*	53:	em_esthum19:*
11:	gb_est11:*	54:	em_esthum20:*
12:	gb_est12:*	55:	em_esthum21:*
13:	gb_est13:*	56:	em_esthum22:*
14:	gb_est14:*	57:	em_esthum23:*
15:	gb_est15:*	58:	em_esthum24:*
16:	gb_est16:*	59:	em_esthum25:*
17:	gb_est17:*	60:	em_esthum26:*
18:	gb_est18:*	61:	em_esthum27:*
19:	gb_est19:*	62:	em_esthum28:*
20:	gb_est20:*	63:	em_estin1:*
21:	gb_est21:*	64:	em_estin2:*
22:	gb_est22:*	65:	em_estin3:*
23:	gb_est23:*	66:	em_estin4:*
24:	gb_est24:*	67:	em_estin5:*
25:	gb_est25:*	68:	em_estoni:*
26:	gb_est26:*	69:	em_estom1:*
27:	gb_est27:*	70:	em_estov1:*
28:	gb_est28:*	71:	em_estov2:*
29:	gb_est29:*	72:	em_estpl1:*
30:	gb_est30:*	73:	em_estpl2:*
31:	gb_est31:*	74:	em_estpl3:*
32:	gb_est32:*	75:	em_estpl4:*
33:	em_estba:*	76:	em_estpl5:*
34:	em_estfun:*	77:	em_estpl6:*
35:	em_esthum1:*	78:	em_estpl7:*
36:	em_esthum2:*	79:	em_estpl8:*
37:	em_esthum3:*	80:	em_estpl9:*
38:	em_esthum4:*	81:	em_estpl10:*
39:	em_esthum5:*	82:	em_estro1:*
40:	em_esthum6:*	83:	em_estro2:*
41:	em_esthum7:*	84:	em_estro3:*
42:	em_esthum8:*	85:	em_estro4:*
43:	em_esthum9:*	86:	em_estro5:*
		87:	em_estro6:*
		88:	em_estro7:*
		89:	em_estro8:*
		90:	em_estro9:*
		91:	em_estro10:*
		92:	em_estro11:*
		93:	em_estro12:*
		94:	em_estro13:*
		95:	em_estro14:*
		96:	em_estro15:*
		97:	em_estro16:*
		98:	em_estro17:*
		99:	em_estro18:*
		100:	em_estro19:*
		101:	em_estro20:*
		102:	gb_est25:*
		103:	gb_est26:*
		104:	gb_est27:*
		105:	gb_est28:*
		106:	gb_est29:*
		107:	gb_est30:*
		108:	gb_est31:*
		109:	gb_est32:*
		110:	gb_est41:*
		111:	gb_est42:*
		112:	gb_est43:*
		113:	gb_est44:*
		114:	gb_est45:*
		115:	gb_est46:*
		116:	gb_est47:*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est67:\*  
137: gb\_est68:\*  
138: gb\_est69:\*  
139: gb\_est70:\*  
140: gb\_est71:\*  
141: gb\_est72:\*  
142: gb\_est73:\*  
143: gb\_est74:\*  
144: gb\_est75:\*  
145: gb\_est76:\*  
146: gb\_est77:\*  
147: gb\_est78:\*  
148: gb\_est79:\*  
149: gb\_est80:\*  
150: gb\_est81:\*  
151: gb\_est82:\*  
152: gb\_est83:\*  
153: gb\_est84:\*  
154: gb\_est85:\*  
155: gb\_est86:\*  
156: gb\_est87:\*  
157: gb\_est88:\*  
158: gb\_est89:\*  
159: gb\_est90:\*  
160: gb\_est91:\*  
161: gb\_est92:\*  
162: gb\_est93:\*  
163: gb\_est94:\*  
164: gb\_est95:\*  
165: gb\_est96:\*  
166: gb\_est97:\*  
167: gb\_est98:\*  
168: gb\_est99:\*  
169: gb\_est100:\*  
170: gb\_est101:\*  
171: gb\_est102:\*  
172: gb\_est103:\*  
173: gb\_est104:\*  
174: gb\_est105:\*  
175: gb\_est106:\*  
176: gb\_est107:\*  
177: gb\_est108:\*  
178: gb\_est109:\*  
179: gb\_est110:\*  
180: gb\_est111:\*  
181: gb\_est112:\*  
182: gb\_est113:\*  
183: gb\_est114:\*  
184: gb\_est115:\*  
185: gb\_est116:\*  
186: gb\_est117:\*  
187: gb\_est118:\*  
188: gb\_est119:\*  
189: gb\_est120:\*

190: gb\_est121:\*  
191: gb\_est122:\*  
192: gb\_est123:\*  
193: gb\_est124:\*  
194: gb\_est125:\*  
195: gb\_est126:\*  
196: gb\_est127:\*  
197: gb\_est128:\*  
198: gb\_est129:\*  
199: gb\_est130:\*  
200: gb\_est131:\*  
201: gb\_est132:\*  
202: gb\_est133:\*  
203: gb\_est134:\*  
204: gb\_est135:\*  
205: gb\_est136:\*  
206: gb\_est137:\*  
207: gb\_est138:\*  
208: gb\_est139:\*  
209: gb\_est140:\*  
210: gb\_est141:\*  
211: gb\_est142:\*  
212: gb\_est143:\*  
213: gb\_est144:\*  
214: gb\_est145:\*  
215: gb\_est146:\*  
216: gb\_est147:\*  
217: gb\_est148:\*  
218: gb\_est149:\*  
219: gb\_est150:\*  
220: gb\_est151:\*  
221: gb\_est152:\*  
222: gb\_est153:\*  
223: gb\_est154:\*  
224: gb\_est155:\*  
225: gb\_est156:\*  
226: gb\_est157:\*  
227: gb\_est158:\*  
228: gb\_est159:\*  
229: gb\_est160:\*  
230: gb\_est161:\*  
231: gb\_est162:\*  
232: gb\_est163:\*  
233: gb\_est164:\*  
234: gb\_est165:\*  
235: gb\_est166:\*  
236: gb\_est167:\*  
237: gb\_est168:\*  
238: gb\_est169:\*  
239: gb\_est170:\*  
240: gb\_est171:\*  
241: gb\_est172:\*  
242: gb\_est173:\*  
243: gb\_est174:\*  
244: gb\_est175:\*  
245: gb\_est176:\*  
246: gb\_est177:\*  
247: gb\_est178:\*  
248: gb\_est179:\*  
249: gb\_est180:\*  
250: gb\_est181:\*  
251: gb\_est182:\*  
252: gb\_est183:\*  
253: gb\_est184:\*  
254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.4	79.0	877	145	BF144493
2	266.4	75.9	1559	145	BF138708
3	260.8	74.3	494	174	BG145342
4	258.6	73.7	404	149	BF452207
5	258.6	73.7	469	23	AL645111
6	258.6	73.7	823	3	AA170256
7	255.8	72.9	886	150	BF582912
8	255	72.6	1012	145	BF142302
9	254.8	72.6	774	150	BF581450
10	254.2	72.4	662	145	BF163874
11	252.6	72.0	650	150	BF579001
12	252.4	71.9	904	145	BF180238
13	251	71.5	913	145	BF162056
14	250.2	71.3	454	121	AW824857
15	244	69.5	862	145	BF143948
16	243.2	69.3	908	145	BF161883
17	243	69.2	718	145	BF136279
18	241.2	68.7	689	150	BF579926
19	240.8	68.6	987	150	BF577496
20	240.4	68.5	940	150	BF580726
21	231.6	66.0	415	113	AW215320
22	231.4	65.9	677	165	BE286624
23	230	65.5	406	115	AW401971
24	229.4	65.4	969	150	BF579260
25	226.2	64.4	511	115	AW402613
26	219.2	62.5	415	9	AA575218
27	219.2	62.5	456	115	AW403059
28	218.2	62.2	440	115	AW408304
29	218	62.1	582	115	AW401386
30	217.6	62.0	1164	172	BF974771
31	216.8	61.8	548	115	AW408295
32	215.8	61.4	991	172	BF974524
33	215.6	61.4	735	106	AL551886
34	215.4	61.4	471	115	AW403220
35	215.2	61.3	964	151	BF663281
36	215	61.3	648	132	BG340670
37	214.2	61.0	678	152	BG340648
38	213.6	60.9	491	115	AW402907
39	212.4	60.5	436	115	AW402311
40	212.2	60.5	687	153	BG397964
41	210.8	60.1	487	115	AW403862
42	210.2	59.9	447	115	AW402793
43	210.2	59.9	510	115	AW403707
44	210	59.8	396	115	AW407843
45	209.2	59.6	518	115	AW402029

ALIGNMENTS

RESULT	1
LOCUS	BF144493
DEFINITION	601790133F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020753 5', mRNA sequence.
ACCESSION	BF144493
VERSION	BF144493.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 877)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES	source
1..877	Location/Qualifiers
1	High quality sequence stop: 644.
1	Plate: LAM9275 row: a column: 10
1	found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
1	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
1	DNA Sequencing by: Incyte Genomics, Inc.
1	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1	Tissue procurement: Gilbert Smith, Ph.D.
1	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>
1	Investigator providing samples: Gilbert Smith, NIH
1	cdt. Library constructed by Life Technologies.
1	MTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
1	Site 2: Salt; transgenic model WNT-1, expression driven by
1	note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
1	/lab_host="DH10B"
1	/tissue_type="tumor, metastatic to mammary"
1	/clone_lib="NCI_CGAP_Lu30"
1	/db_xref="taxon:10090"
1	/strain="C2EHC II"
1	/organism="Mus musculus"
1	192 t
198 a	233 c
233 c	254 g
254 g	192 t
BASE COUNT	198 a 233 c 254 g 192 t
ORIGIN	
Query Match	79.0%; Score 277.4; DB 145; Length 877;
Best Local Similarity	90.4%; Pred. No. 4.4e-75;
Matches 319; Conservative	0; Mismatches 31; Indels 3; Gaps 2;
QY 1	GAAGTCACGCTGGTGAGCTGGGGAGGCTAGTGAAGCTGGAGGCTCCCTGAGACATC 60
DB 95	GAGGTCACGCTGGTGAGCTGGGGAGGCTAGTGAAGCTGGAGGCTCCCTGAAACATC 154
QY 61	TCTGTGACGCTCTGGATTGCTTTTCAGTAGCTATGACATGTCTTTGGTTCGCCAGATT 120
DB 155	TCTGTGACGCTCTGGATTGCTTTTCAGTAGCTATGACATGTCTTTGGTTCGCCAGATT 213
QY 121	CCGGAGAGAGCTGGAGTGGGTGCGCAAAAGTAGTAGTGGTGGTGGTGGTGGTGGTGGT 180
DB 214	CCAGACAGAGGCTGGAGTGGGTGCGCAAAAGTAGTAGTGGTGGTGGTGGTGGTGGTGGT 273
QY 181	TTAGACACTGTGAGGCGCGATTCCACATCTCCAGAGACAATGCCAAGAACCCCTATAC 240
DB 274	CCAGACAGTGTGAGGCGCGATTCCACATCTCCAGAGACAATGCCAAGAACCCCTATAC 333
QY 241	CTGCAATGAGCAGTCTGAACCTGTGAGGACACAGCCATGTATTACTGTGCAAGACA--TA 298
DB 334	CTGCAATGAGCAGTCTGAAGCTGTGAGGACACAGCCATGTATTACTGTGCAAGCCAGGG 393
QY 299	ACTACGCGAGTTTGGCTTACTGGGCGCAAGGACTCTGCTGCTGCTGCTGCTGCTGCTGCA 351
DB 394	GTTCAGACCCGTTTGGCTTACTGGGCGCAAGGACTCTGCTGCTGCTGCTGCTGCTGCTGCA 446
RESULT	2
LOCUS	BF138708
DEFINITION	601781893F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009847 5', mRNA sequence.
ACCESSION	BF138708
VERSION	BF138708
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1559)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)













```
QY 241 CTGCAATGAGCAGTCTGAACCTCTGAGGACACAGCCATCTATTACTGTGCAAGACATAC 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 368 CTGCAGATGAGCAGTCTGAGGCTCTGAGGACACAGCCTTGTATTACTG-----GTGCAAGA 422
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 301 TAGGCGAGTTTTCCTACTTGGGGCCAAAGGACTCTGGTCACATGCTCTCTGCA 351
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 423 CATCTGACTATGACTTGGGGTCAAGGAACCTCAGTCACCGCTCTCTCTCA 473
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 12
BF180238 904 bp mRNA EST 31-OCT-2000
LOCUS 601806516r1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4037595 5',
DEFINITION mRNA sequence.
ACCESSION BF180238
VERSION BF180238
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9314 row: 0 column: 04
High quality sequence stop: 723.
FEATURES
source
1. 904
/organism="Mus musculus"
/db_stain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:4037595"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 208 a 228 c 239 g 228 t 1 others
ORIGIN

Query Match 71.9%; Score 252.4; DB 145; Length 904;
Best Local Similarity 85.9%; Pred. No. 2.5e-67;
Matches 304; Conservative 0; Mismatches 46; Indels 4; Gaps 2;

QY 1 GAAGTCAGCTGGTGGGAGCTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCGAGACTC 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 117 GAAGTGAAGTTGGTGGAGTCTGGGGGAAG-TTTGTGACGCCCTGGAGGTCCTCGAACTC 175
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 TCCTGTGCAGCCTCTGGATTCGCTTCAGTACGTATGACATGCTTGGGTTCGCCAGATT 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 176 TCCTGTGCAGCCTCTGGATTCGCTTCAGTACGTATGACATGCTTGGGTTCGCCAGACT 235
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 121 CCGGAGAAGAGGCTGGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGTGGTACGACCTACTAT 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 236 CCAGAGAAAAGGCTGGAGTGGGTTCGCAAGATTAGTTCTGGTGGTGCATACTATTACTAT 295
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 181 TTAGACACTGTGCAGGGCCGATTACCAATCTCCAGAGACAATGCCAAGAACCCCTATAC 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

```
Db 296 CTAGACATTATAAAGGCGGATTACCATCTCCAGAGACAATGTCAAGAACATTCCTGTAT 355
QY 241 CTGCAATGAGCAGTCTGAACCTCTGAGGACACAGCCATCTATTACTGTGCAA---GACAT 297
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 356 CTGCAATGAACAGTCTGAAGTCTGAGGACAGGCCACATATTTACTGTCAAGTGGAGAT 415
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 298 AACTACGGCAGTTTTCCTACTTGGGGCCAAAGGACTCTGGTCACATGCTCTCTGCA 351
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 416 GATGAGCCTGGTTTGTACTTGGGGCCAAAGGACTCTGGTCACATGCTCTCTGCA 469
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 13
BF162056 913 bp mRNA EST 30-OCT-2000
LOCUS 601768714F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3987986 5',
DEFINITION mRNA sequence.
ACCESSION BF162056
VERSION BF162056
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 913)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9195 row: 1 column: 03
High quality sequence stop: 581.
FEATURES
source
1. 913
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3987986"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 218 a 248 c 260 g 187 t
ORIGIN

Query Match 71.5%; Score 251; DB 145; Length 913;
Best Local Similarity 85.3%; Pred. No. 6.7e-67;
Matches 308; Conservative 0; Mismatches 40; Indels 13; Gaps 2;

QY 1 GAAGTCAGCTGGTGGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCGAGACTC 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 127 GAAGTCAGCTGGTGGAGTCTGGGGAAACTTAGTGAAGCCCTGGAGGTCCTCGAAACTC 186
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 61 TCCTGTGCAGCCTCTGGATTCGCTTCAGTACGTATGACATGCTTGGGTTCGCCAGATT 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 187 TCCTGTGCAGCCTCTGGATTCGCTTCAGTACGTATGACATGCTTGGGTTCGCCAGACT 246
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 121 CCGGAGAAGAGGCTGGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGTGGTACGACCTACTAT 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 247 CCGGAGAAGAGGCTGGAGTGGGTTCGCAAGATTAGTTCTGGTGGTGGTACGACCTACTAT 303
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 181 TTAGACACTGTGCAGGGCCGATTACCAATCTCCAGAGACAATGCCAAGAACCCCTATAC 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

Db 304 CCAGACAGTGTGAAGGGTCGATTCCACCATCTCCAGAGACAAGGCCAAGACACCTGTAC 363  
QY 241 CTGCAAAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTATCTGCGAAGAC- - - - 295  
Db 364 CTCAAAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTATCTGCGAAGACGTGGT 423  
QY 296 - - - - - ATAACTACGCGAGTCTTTGGTTACTGGGGCCAAAGGACTCTGGTCACTGCTCTGC 350  
Db 424 GGTTACTACGATGGTACTTCCGATGTCTGGGGCCAGGACCACGGTCAACCGTCTCTCTC 483  
QY 351 A 351  
Db 484 A 484

RESULT 14  
AW824857  
LOCUS  
DEFINITION  
us08col.y1 Soares\_NMGBC\_B-cell Mus musculus cDNA clone  
IMAGE:3166464 5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR  
V-III REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID  
immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 454)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

MGI:1061924

Seq primer: -40RP from Gibco.

Location/Qualifiers

1..454

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="IMAGE:3166464"

/clone\_lib="Soares.NMGBC\_B-cell"

/tissue\_type="germinal B-cell from resting spleen"

/lab\_host="DH10B (phage resistant)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: NotI; Site\_2: EcoRI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5',

TGTTACCAATCTGAAGTGGAGCGCGCGAGGATTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pT73 vector. Library

constructed and normalized by Bento Soares and M.Fatima

Bonaldo."

BASE COUNT 102 a 109 c 127 g 116 t

ORIGIN

Query Match 71.3%; Score 250.2; DB 121; Length 454;

Best Local Similarity 85.1%; Pred. No. 9.9e-67;

Matches 292; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 1 GAAGTCAGCTGTGGAGTCTGGGGAGGCTTAGTAGAGCTGGAAGGCTCCCTGAGACTC 60

Db 112 GAGGTGACGTGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGCTCCTGAAACTC 171  
QY 61 TCCTGTGACGCTCTGGATTCGCTTTCAGTAGCTATGACATGTCTTGGGTTCGCCAGATT 120  
Db 172 TCCTGTGACGCTCTGGATTCACCTTTCAGTGACTATGGAATGCGACTGGTTCGTCAGGCT 231  
QY 121 CCGGAGAAGAGGCTGGAGTGGTCGCAAAAGTTAGTAGTGGTGGTAGGCACCTACTAT 180  
Db 232 CCAGAGAAGGCTGGAGTGGTGGTTCATACATTAGTAGTGCAGTAGTACCATTACTAT 291  
QY 181 TTAGACACTGTGCGAGGCGGANTTCCCATCTCCAGAGACAAATGCCAAGAACACCCCTATAC 240  
Db 292 GCAGACACAGTGAAGGCGCGATTTCACCATCTCCAGAGACAAATGCCAAGAACACCCCTGTC 351  
QY 241 CTGCAAAATGAGCAGTCTGAACCTCTGAGGACACACCCATGTATTACTGTGCAAGAC- - - AT 297  
Db 352 CTGCAAAATGAGCAGTCTGAGTCTGAGGACACGCGCATGTATTACTGTGCAAGCCCGGG 411  
QY 298 AACTACGCGCAGTTTGGTTACTTGGGGCCAAAGGACTCTGGTCA 340  
Db 412 GGTTCCTCTGGTTGCTTACCTGGGCGCAAGGACTCTGGTCA 454

RESULT 15  
BF143948  
LOCUS  
DEFINITION  
601786493F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4014430 5',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 862)  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9258 row: i column: 23  
High quality sequence stop: 671.

FEATURES  
source  
1..862  
/organism="Mus musculus"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4014430"  
/clone\_lib="NCI\_CGAP\_Lu30"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/notes="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; transgenic model WNT-1, expression driven by  
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
dT. Library constructed by Life Technologies."  
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 213 a 236 g 176 t 1 others  
ORIGIN

Query Match 69.5%; Score 244; DB 145; Length 862;  
Best Local Similarity 82.7%; Pred. No. 9.7e-65;  
Matches 291; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

```

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60
Db 99 GAGGTGCACCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGTCCTCCGGAACCTC 158
QY 61 TCCTGTGCAGCCTCTGGATTCTTCAGTAGCTATGACATGTCTTGGGTTCCGCCAGATT 120
Db 159 TCCTGTGCAGCCTCTGGATTCTTCAGTAGCTATGGAATGCACCTGGGTTCCGTCAGGCT 218
QY 121 CCGGAGAAGAGCTGGAGTGGGTCCGAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180
Db 219 CCAGAGAAGGGCTGGAGTGGGTGGCATACATTAGTAGTGGCAGTAGTACCATCTACTAT 278
QY 181 TTAGACTGTGTCAGGGCCGATTACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240
Db 279 GCAGACACAGTGAAGGGCCGATTACCATCTCCAGAGACAATGCCAAGAACACCCCTGTT 338
QY 241 CTGCAAAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAAC 300
Db 339 CTGCAAAATGACCAGTCTAAGGCTCTGAGGACACGGCCATGTATTACTGTGCAAGGCCAGGT 398
QY 301 TACGGCAGT-TTTGCTTACTGGGGCCAGGGACTCTGGTCACTGTCTCTGCA 351
Db 399 TACTCCCTATCGGACTACTGGGGTCAGGAACCTCAGTCACCGTCTCTCTCA 450

```

Search completed: October 11, 2001, 14:34:04  
Job time: 5541 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:36 ; Search time 177.65 seconds  
(without alignments)  
1240.605 Million cell updates/sec

Title: US-08-791-391A-5

Perfect score: 351

Sequence: 1 GAAGTGCAGCTGGTGGAGTC.....CTCTGCTACTGCTCTGTCA 351

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N\_Geneseq\_0601.\*
- 1: /SIDSI/gcgdata/geneseq/geneseq/NA1980.DAT.\*
  - 2: /SIDSI/gcgdata/geneseq/geneseq/NA1981.DAT.\*
  - 3: /SIDSI/gcgdata/geneseq/geneseq/NA1982.DAT.\*
  - 4: /SIDSI/gcgdata/geneseq/geneseq/NA1983.DAT.\*
  - 5: /SIDSI/gcgdata/geneseq/geneseq/NA1984.DAT.\*
  - 6: /SIDSI/gcgdata/geneseq/geneseq/NA1985.DAT.\*
  - 7: /SIDSI/gcgdata/geneseq/geneseq/NA1986.DAT.\*
  - 8: /SIDSI/gcgdata/geneseq/geneseq/NA1987.DAT.\*
  - 9: /SIDSI/gcgdata/geneseq/geneseq/NA1988.DAT.\*
  - 10: /SIDSI/gcgdata/geneseq/geneseq/NA1989.DAT.\*
  - 11: /SIDSI/gcgdata/geneseq/geneseq/NA1990.DAT.\*
  - 12: /SIDSI/gcgdata/geneseq/geneseq/NA1991.DAT.\*
  - 13: /SIDSI/gcgdata/geneseq/geneseq/NA1992.DAT.\*
  - 14: /SIDSI/gcgdata/geneseq/geneseq/NA1993.DAT.\*
  - 15: /SIDSI/gcgdata/geneseq/geneseq/NA1994.DAT.\*
  - 16: /SIDSI/gcgdata/geneseq/geneseq/NA1995.DAT.\*
  - 17: /SIDSI/gcgdata/geneseq/geneseq/NA1996.DAT.\*
  - 18: /SIDSI/gcgdata/geneseq/geneseq/NA1997.DAT.\*
  - 19: /SIDSI/gcgdata/geneseq/geneseq/NA1998.DAT.\*
  - 20: /SIDSI/gcgdata/geneseq/geneseq/NA1999.DAT.\*
  - 21: /SIDSI/gcgdata/geneseq/geneseq/NA2000.DAT.\*
  - 22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	351	100.0	351	19	AAV49822
2	351	100.0	351	22	AAV28177
3	309.4	88.1	482	11	AAQ05555
4	302.2	86.1	351	19	AAQ05820
5	302.2	86.1	351	22	AAV28175
6	296.6	84.5	413	15	AAQ06850
7	293.6	83.6	721	20	AAV99765
8	293.6	83.6	721	21	AAV37397
9	293.6	83.6	733	20	AAV99766
10	293.6	83.6	733	21	AAV37398
11	291	82.9	369	19	AAV07642
					LM609 antibody hea
					Antibody LM609 hea
					Sequence encoding
					Vitaxin antibody h
					Vitaxin heavy chai
					MAB A33 heavy chai
					A33/212 single-cha
					Linked fusion prot
					A33/218 single-cha
					Linked fusion prot
					anti-CD22 monoclon

12	289.6	82.5	1938	19	AAV58929	A33 chimeric recep
13	284	80.9	418	15	AAQ62764	Murine KC-4 immuno
14	284	80.9	418	15	AAQ62789	Murine KC-4 immuno
15	283.6	80.8	411	19	AAV24232	Chimeric antibody
16	283.6	80.8	411	20	AAQ00092	Mouse humanised an
17	283.6	80.8	411	21	AAZ58913	Mouse antibody H c
18	283.6	80.8	411	22	AAV69129	Human PTHrp mouse
19	283.6	80.8	411	22	AAV69185	Human PTHrp mouse
20	283.6	80.8	411	22	AAV69241	Human PTHrp mouse
21	282.4	80.5	441	18	AAV72269	Chimeric MAB 15 PC
22	282.2	80.4	480	13	AAQ20070	MRK16-H chain. Ch
23	280.8	80.0	457	18	AAV72267	Mouse MAB 15 heavy
24	277.4	79.0	357	15	AAQ66409	VH coding region o
25	274.6	78.2	417	15	AAQ62804	Humanised murine K
26	274.6	78.2	417	16	AAQ87534	Humanised anti-KC-
27	271.6	77.4	351	16	AAQ6282	Human Ige receptor
28	271.6	77.4	351	16	AAQ96284	Human Ige receptor
29	271.6	77.4	351	18	AAV90025	cDNA encoding heav
30	271	77.2	445	14	AAQ36530	Chimeric MAB heavy
31	271	77.2	445	14	AAQ36537	BR55-2 heavy chain
32	271	77.2	491	14	AAQ36535	BR55-2 murine IgG3
33	269.4	76.8	923	16	AAV51436	B cell hybridoma 1
34	268.8	76.6	324	13	AAQ20303	Antibody 4A2 heavy
35	268.6	76.5	426	14	AAQ34576	15D3 antibody heav
36	267.8	76.3	357	19	AAV44997	15D3 VH chain codi
37	267.8	76.3	357	20	AAZ10957	Antibody 15D3 hea
38	267.8	76.3	357	20	AAV08933	Antibody 3S193 hea
39	266.2	75.8	357	16	AAV04997	B5 immunoglobulin
40	266.2	75.8	357	17	AAV28000	Lewis-Y antibody B
41	264.6	75.4	899	17	AAV16700	Plasmid pD17-cj-dC
42	264.6	75.4	8327	19	AAV18597	Plasmid expressing
43	264.6	75.4	8691	19	AAV18696	Pv(TU25). Homo sa
44	263.6	75.1	717	14	AAQ40463	Lewis-Y antibody B
45	263	74.9	357	17	AAV16699	

## ALIGNMENTS

RESULT 1

AAV49822 AAV49822 standard; DNA; 351 BP.

XX AC AAV49822;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 antibody heavy chain variable region DNA fragment.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; ss.

XX OS Mus sp.

XX PH Key Location/Qualifiers

XX FT CDS 1..351

XX FT /\*tag= a

XX FT /product= "LM609 antibody heavy chain variable region"

XX FT /note= "partial sequence, no start or stop codon given"

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX



```

XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 75..482
XX FT /*tag= a
XX PN EP380068-A.
XX PD 01-AUG-1990.
XX PF 24-JAN-1990; 90EP-0101351.
XX PR 04-DEC-1989; 89US-04411702.
XX PR 24-JAN-1989; 89US-0301216.
XX PA (MOLE-) MOLECULAR THERAPEU.
XX PI Zerler B;
XX WPI; 1990-232892/31.
XX P-PSDB; AAR06251.
XX Expression vectors for producing chimeric monoclonal antibodies -
XX PT which express human constant region and non-human variable region
XX PS Disclosure; ; p; English.
XX CC MABs comprising mouse CH and CL constant regions which human
XX CC variable regions may be used to create mouse/human hybrid MABs,
XX CC which have a longer serum half-life. Method can be used to produce
XX CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX SQ Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;

Query Match 88.1%; Score 309.4; DB 11; Length 482;
Best Local Similarity 92.6%; Pred. No. 1.2e-82;
Matches 325; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGTGGAGCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60
DB 132 gaagtcagctgtggagctggggaggttagtgaagcctggaagctggaggtccctgaaactc 191
QY 61 TCCTGTGACGCTCTGATTCGCTTTCAGTAGCTATGACATGCTGCTGGTTCGCCAGATT 120
DB 192 tctgtgacgctctggttcgcttcttcagtagcattgacatgctctgggttcgccagact 251
QY 121 CCGGAGAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTGGTGGTGGTGGTGGT 180
DB 252 ccggagaagagctggagtggtgctgcatacattagtagtggtggtgatacacctactat 311
QY 181 TTAGACACTGTGAGGCGCCGATTACCATCTCCAGAGACATGCCAAGACACCCCTATAC 240
DB 312 ccagacactgtgaaggccgagctaccatctccagagacatgccaagaacaccccttac 371
QY 241 CTGCAATGAGCAGCTGGAAGCTCTGAGGACACAGCCATGATTACTGTGCAAGACATAAC 300
DB 372 ctgcaaatgagcagctggaagctctgagacacagccgtgtattactgtgaagaaggtac 431
QY 301 TAGCGGAGTTTGTACTGGGCGCAAGGACTGTGTGCTACTGTCTGTGCA 351
DB 432 ggctccctttgttactggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 482

RESULT 4
AAV49820
ID AAV49820 standard; DNA; 351 BP.
XX AC AAV49820;
XX XX
XX 02-NOV-1998 (first entry)
XX

```

---

```

DE XX Vitaxin antibody heavy chain variable region DNA.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 1..351
XX FT /*tag= a
XX FT /product= "vitaxin antibody heavy chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"
XX PN WO9833919-A2.
XX XX
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI; 1998-437472/37.
XX DR P-PSDB; AAW76001.
XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX PS Claim 3; Fig 1a; 129pp; English.
XX CC This sequence encodes the vitaxin antibody variable heavy chain region.
XX CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
XX CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX CC block integrin-mediated signal transduction. This is useful in the
XX CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX CC etc.). The antibodies contain non-murine framework regions so are
XX CC suitable for use in humans. Enhanced types of LM609 have affinity more
XX CC than 90 times greater than that of parent the parent antibody.
XX SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 86.1%; Score 302.2; DB 19; Length 351;
Best Local Similarity 91.9%; Pred. No. 1.5e-80;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AAGTGCAGCTGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTCT 61
DB 2 aggtgcagctgtggagctggggagggcgctgtgcagcctgggaaggtccctgagactct 61
QY 62 CCTGTGCAGCCTCTGGATTTCGCTTTTCAGTAGCTATGACATGCTTGGGTTCCGCCAGATT 121
DB 62 cctgtgcagcctctggatttcgcttttcagtagctatgacatgcttgggttcgccagactc 121
QY 122 CGGAGAAAGAGCTGGAGTGGGTGCGAAAGTTAGTGGTGGTGGTGGTGGTGGTGGTGGT 181
DB 122 cgggaaagagctggagtggttcgcaaaagttagtagtggtgggttagcaccctactatt 181
QY 182 TAGACACTGTGACAGGCGCGGATTTCACCATCTCCAGAGACATGCCAAGACACCCCTATAC 241
DB 182 tagacactgtgacagggcggttcacccatctccagagacaatagtagaagaacacccctacc 241

```

QY 242 TGC AATGACGACTGTGAACCTTGAGGACACAGCCATGTATTACTGTGCAAGACATAACT 301  
 Db 242 tgcaaatgaacttctgagagccgagacacagccgtgtattactgtgcaagacataact 301  
 QY 302 ACGGCACTTTTCTTACTGGGCCAAGGACACTGTGTCACCTGCTCT 348  
 Db 302 acggcagcttttcttactgggccaaggagactacagtgactgtttct 348  
 RESULT 5  
 AAF28175  
 ID AAF28175 standard; DNA; 351 BP.  
 AC AAF28175;  
 XX  
 DT 03-APR-2001 (first entry)  
 DE Vitaxin heavy chain variable region DNA.  
 KW LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis.  
 XX  
 PS Disclosure; Fig 1; 132pp; English.  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;  
 Query Match 86.1%; Score 302.2; DB 22; Length 351;  
 Best Local Similarity 91.9%; Pred. No. 1.5e-80;  
 Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
 QY 2 AAGTCAGCTGTGGAGCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTGAGACTCT 61  
 Db 2 aggtcagctgtgtgagctggggaggcggtgtgtcagcctggaggtccctgagactct 61  
 QY 62 CTGTGACGCCCTGTGATTCGGTCTTTCAGTAGCTATGACATGTCTGGGTTCGCCAGATTC 121  
 Db 62 cctgtgacgcctctgattcaccttcagtagctatgacatgtctgggttcgccaggctc 121  
 QY 122 CGGAGAGAGGCTGGAGTGGGTGCGGAAAGTTAGTAGTGGTGGGTAGCAGCTACTATT 181

Db 122 cgggcaaggctgtgagtggtgcgaaaagttagtagtggtgtagcactactatt 181  
 QY 182 TAGACACTGTGAGGCGCATTCACCATCTCCAGAGACAATGCCAAGACACCCCTATACC 241  
 Db 182 tagacactgtgcaggcgagattccacatctccagagacaatagtaagaacacccctatacc 241  
 QY 242 TGC AATGACGACTGTGAACCTTGAGGACACAGCCATGTATTACTGTGCAAGACATAACT 301  
 Db 242 tgcaaatgaacttctgagagccgagacacagccgtgtattactgtgcaagacataact 301  
 QY 302 ACGGCACTTTTCTTACTGGGCCAAGGACACTGTGTCACCTGCTCTCT 348  
 Db 302 acggcagcttttcttactgggccaaggagactacagtgactgtttct 348  
 RESULT 6  
 AAQ68650  
 ID AAQ68650 standard; DNA; 413 BP.  
 AC AAQ68650;  
 XX  
 DT 13-FEB-1995 (first entry)  
 DE MAb A33 heavy chain coding sequence.  
 KW Polymerase chain reaction; primer; amplify; PCR; variable region; light;  
 KW heavy; chains; VL; VH; humanised; antibody; vectors; expression; human;  
 KW secretion; A33; Fab'(gamma/delta/cys); PGL6; ompa signal; C-kappa;  
 KW pSKompa; PMR055; CH1 domains; hinge; deltaCys; PMR022; PRO109;  
 KW antigen; diagnosis; treatment; colorectal cancer; metastases; ss.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT primer\_bind 1..32 /\*tag= a  
 FT CDS 6..413 /\*tag= b  
 FT sig\_peptide 6..62 /\*tag= c  
 FT mat\_peptide 63..413 /\*tag= d  
 FT primer\_bind 396..413 /\*tag= e  
 XX  
 PN WO9413805-A.  
 XX  
 PD 23-JUN-1994.  
 PF 10-DEC-1993; 93WO-GB02529.  
 PR 10-DEC-1992; 92GB-0025853.  
 PR 22-JUL-1993; 93GB-0015249.  
 XX  
 PA (CLIT ) CELLTech LTD.  
 XX  
 PI Adair JR, King DJ, Owens RJ;  
 XX  
 DR WPI; 1994-217881/26.  
 DR P-PSDB; AAR56962.  
 XX  
 PT Humanised antibodies raised against A33 antigen - are used for  
 PT diagnosis or treatment of colorectal tumours and metastases  
 XX  
 PS Example 1; Fig 3(ii); 90pp; English.  
 CC The sequences given in AAQ68649-50 encode the light and heavy chain  
 CC variable regions (VH and VL) of the humanised anti-A33 antibody of  
 CC the invention. These fragments were produced by PCR using the primer  
 CC sequences given in AAQ68624-48. The amplified fragments were used in  
 CC the construction of vectors for the expression and secretion of the

CC chimeric humanised A33. The amplified products were cleaved with BstBI  
 CC and SphI for the light chain and HindIII and ApaI for the heavy chain.  
 CC These fragments were cloned into the human kappa light chain acceptor  
 CC vector, pMR15.1, and the human heavy chain, IgG1, acceptor vector,  
 CC pMR1011 respectively, to give chimeric expression vector pRO108 for the  
 CC light chain and pRO107 for the heavy chain. Proteins which bind the A33  
 CC antigen can be used in the diagnosis or treatment of colorectal cancers  
 CC and metastases.

XX  
 SQ Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;

Query Match 84.5%; Score 296.6; DB 15; Length 413;  
 Best Local Similarity 90.3%; Pred. No. 7.2e-79;  
 Matches 317; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGTGGAGCTGGGGAGGCTTGTAGTGAAGCTGGAGGTCCTCGAGACTC 60  
 DB 63 gaagtgaagctggtgagctgggagggccttagtagaagcctggagggctcctgaaactc 122  
 QY 61 TCCTGTGACGCTCTGATTCGCTTTTCAGTATGACATGCTTGGGTTCCGCCAGATT 120  
 DB 123 tctctgtgcgctctgagctgttccttcagtcacctagacatgcttgggtctgcgcgact 182  
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180  
 DB 183 ccggaagaagcgtgagtggtggtgcgaaccattagtagtggtgtgtacacctactat 242  
 QY 181 TTAGACACTGTGCGAGGCGGATTCACATCTCCAGAGACAAATGCCAAGAACCCCTATAC 240  
 DB 243 ttgacagagtgaaggccgattcaacctctccagagacagtgccaggaaacacctatac 302  
 QY 241 CTGCAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGATTACTGTGCAACACATAC 300  
 DB 303 ctgcaaatgagcagctgagtgctgaggacacggccttattactgtgcagcactacg 362  
 QY 301 TAGCGCAGTTTCTTACTGAGGCGCCAGGAGCTCTGGTACTGCTCTCTGCA 351  
 DB 363 gtagtcccgcttcttactgaggccagggaactctggtcaccgtctctgca 413

RESULT 7

AAV99765  
 ID AAV99765 standard; DNA; 721 BP.

AAV99765;

23-MAR-1999 (first entry)

A33/212 single-chain Fv coding sequence.

Linker: fusion polypeptide; proteolysis: subtilisin; trypsin; scFv;  
 multi-chain protein; immunoglobulin; single chain antibody Fv; cancer;  
 aggregation; ds.

Synthetic.

Key Location/Qualifiers

CDS 1..711

/tag- a

/product- "A33/212 scFv"

/note- "the start codon is not indicated"

misc\_feature 1..321

/tag- b

/note- "sequence coding for A33 V1 region"

misc\_feature 322..363

/tag- c

/note- "sequence coding for peptide linker 212"

misc\_feature 364..708

/tag- d

/note- "sequence coding for A33 Vh region"

US5856456-A.

XX 05-JAN-1999.  
 PD  
 XX  
 PF 07-APR-1994; 94US-0224591.  
 XX  
 PR 07-APR-1994; 94US-0224591.  
 PR 20-NOV-1992; 92US-0980529.  
 PR 15-JAN-1993; 93US-0002845.  
 XX  
 PA (ENZO-) ENZON INC.  
 XX  
 PI Filpula DR, Whitlow MD;  
 XX  
 DR WPI: 1999-105193/09.  
 DR P-PSDB; AAW95440.  
 XX  
 XX DNA encoding fusion polypeptide including protease resistant linker  
 PT - for making single-chain Fv antibody fragments, e.g for diagnosis  
 PT and treatment of cancer  
 XX  
 PS Disclosure; Fig 12; 39pp; English.  
 XX

CC The invention is directed to a novel peptide linker useful for connecting  
 CC polypeptide constituents into a novel linked fusion polypeptide. The  
 CC peptide linker includes at least one XP motif (where X is a charged  
 CC amino acid) and includes any of these sequences (GSTSGXPGSGSGEGSTKG;  
 CC GTSGSGXPGSGSTKG; or GSTSGKSEGGK) to inhibit its proteolysis by  
 CC subtilisin or trypsin. DNA molecules encoding fusion polypeptides  
 CC containing two polypeptides, derived from the same multichain protein of  
 CC the immunoglobulin (Ig) superfamily and a peptide linker as above, are  
 CC particularly used to prepare single chain antibody Fv fragments (scFv),  
 CC potentially useful for diagnosis and treatment of cancer. The fusion  
 CC polypeptide containing the specified linkers is proteolytically stable  
 CC (associated with positioning of the P residue) and resistant to  
 CC aggregation, while residue X improves solubility. The present sequence  
 CC represents the nucleotide sequence of a A33/212 scFv fragment.

XX Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;

Query Match 83.6%; Score 293.6; DB 20; Length 721;

Best Local Similarity 90.2%; Pred. No. 6.6e-78;

Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGTGGAGCTGGGGAGGCTTAGTGAAGCTGGAAGGTCCTCGAGACTC 60  
 DB 364 gaagtgaagccttgtagtctgggagggccttagtagaagcctggagggctcccgaaactc 423  
 QY 61 TCCTGTGACGCTCTGATTCGCTTTTCAGTATGACATGCTTGGGTTCCGCCAGATT 120  
 DB 424 tctctgtgcgctctgagctgttccttcagtcacctatgacatgctctgtggtcgccagact 483  
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180  
 DB 484 ccggagaagaagcctgagtggtggtcgcaaccattagtagtggtggtgtacacctactat 543  
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAAATGCCAAGAACCCCTATAC 240  
 DB 544 ttgacagagtgaaggccgattcaacctctccagagacagtgccaggaaacacctatac 603  
 QY 241 CTGCAATGAGCAGTCTGAACCTCTGAGGACACAGCCATGATTACTGTGCAAGACATAC 300  
 DB 604 ctgcaaatgagcagctgagtggtggtgaggaacggccttattactgtgcagcactacg 663  
 QY 301 TAGCGCAGTTTCTTACTGAGGCGCCAGGAGCTCTGGTACTGCTCTCT 348  
 DB 664 gtagtcccgcttcttactgaggccagggaactctggtcactgtctct 711

RESULT 8

AAZ37397

ID AAZ37397 standard; DNA; 721 BP.

XX

```
AC AA237397;
XX
XX
DT 08-FEB-2000 (first entry)
XX
XX Linked fusion protein A33/212 sfv coding sequence.
DE
XX Fusion protein; linker; linked fusion polypeptide; multichain protein;
KW protein complex; antibody; ss.
XX
XX Synthetic.
XX
XX US5990275-A.
PN
XX
XX 23-NOV-1999.
PD
XX
XX 10-SEP-1997; 97US-0926789.
PF
XX
XX 07-APR-1994; 94US-0224591.
PR
XX 20-NOV-1992; 92US-0980529.
PR
XX 15-JAN-1993; 93US-0002845.
XX
XX (ENZO-) ENZON INC.
PA
XX
XX Filpula DR, Whitlow MD;
PI
XX WPI; 2000-022812/02.
DR
XX
XX Peptide linkers, linked fusion polypeptides containing the linkers and
PT their preparation -
PT
XX
XX Example; Fig 12; 42pp; English.
PS
XX
XX This sequence encodes a linked fusion protein containing the
CC amino acid linker of the invention. The linkers are used for connecting
CC constituent polypeptides to form novel linked fusion polypeptides.
CC Polypeptides derived from any protein can be connected, in particular
CC multichain protein or protein complexes e.g. enzymes, members of the
CC immunoglobulin superfamily, hormones, DNA-binding proteins. The linker
CC provides fusion proteins which have greater stability and are less
CC susceptible to aggregation.
XX
XX Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;

Query Match 83.6%; Score 293.6; DB 21; Length 721;
Best Local Similarity 90.2%; Pred. No. 6.6e-78;
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTGAGACTC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
364 gaagtgaagcttggagctggggaggcttagtgaagccctggagggtccctgaaactc 423
QY 61 TCCTGTGCAGCTCTGGATTGCTTTCAGTAGCTATGACATGCTTGGGTTCGCCAGATT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
424 tcctgtgagcctcggatcgtcttcagtagctatgacatgcttgggttcgccagact 483
QY 121 CCGGAGACAGAGCTGGAGTGGTGCAGAAAGTTAGTGGTGGTGGTGGTGGTGGTGGT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
484 ccgagagagagctgagtgagggtcgaaccattagtagtggtgtagttacacttactat 543
QY 181 TTAGACACTGTGCAGGGCGGATTCACATCTCCAGAGACAAATGCCAAGAACACCTATAC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
544 ttgacagtgtagaggccgattccaccattctccagagacagtgccaggaaacacctatac 603
QY 241 CNGCAANTGACAGCTGACACTCTGACACACAGCCAGTATTACTGTGCAAGACATAAC 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
604 ctgcaaaatgagcagcttgaggtctgaggacacgacctgtattactgtgaccactgactac 663
QY 301 TACGCAGCTTTGCTTACTGGGCCCAAGGACTCTGGTCACTGTCTCT 348
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
664 gtatcccgcttctgcttacttggggccaaggactctggtcactgtctct 711
```

Query Match

83.6%; Score 293.6; DB 20; Length 733;

Best Local Similarity 90.2%; Pred. No. 6.6e-78;  
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCGAGCTGGTGGAGCTCTGGGGAGGCTTAGTGAAGCCTGGAGCTCCCTGAGACTC 60  
Db 376 gaagtgaagctctgaggagctctggggagggcttagtgaagcctggagggtccctgaaactc 435  
QY 61 TCCGTGTCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTGTGGTTTCGCCAGATT 120  
Db 436 tccgtgcagcctctggatctgctttcagtagcctatgacatgtctgggttcgccagact 495  
QY 121 CCGAGAGAGGCTGGAGTGGGTGCAGAAAGTTAGTAGTGTGGTGGTAGCACTACTAT 180  
Db 496 ccgagagaagggctggagtggtgcgaaccattagtagtggtgtagttacacctactat 555  
QY 181 TTAGACACTGTGTCAGGCGCGATTTCACCATCTCCAGAGACAATGCCAAGAACACCTATAC 240  
Db 556 ttagacagtgtgaagggccgattcaccatctccagagacagtgccagaaacacctatac 615  
QY 241 CTGCAATGAGCACTCTGAACCTCTGAGACACAGCCATGTATTACTGTGCAAGACATAAC 300  
Db 616 ctgcaaatgacagctctgaggtctgagacacgacctgtattactgtgcaccgactacg 675  
QY 301 TACGGCAGTTTGTCTTACTGGGGCCAGGGACTCTGGTCACTGTCTCT 348  
Db 676 gtatgccgtttgtctactgggcccaggagactctgtgtcactgtctct 723

RESULT 10  
AAZ37398  
ID AAZ37398 standard; DNA; 733 BP.  
XX  
AC AAZ37398;  
XX  
DT 08-FEB-2000 (first entry)  
XX  
DE Linked fusion protein A33/218 sFv coding sequence.  
XX  
KW Fusion protein; linker; linked fusion polypeptide; multichain protein;  
KW protein complex; antibody; ss.  
XX  
OS Synthetic.  
XX  
PN US5990275-A.  
XX  
PD 23-NOV-1999.  
XX  
PF 10-SEP-1997; 97US-0926789.  
XX  
PR 07-APR-1994; 94US-0224591.  
PR 20-NOV-1992; 92US-0980529.  
PR 15-JAN-1993; 93US-0002845.  
XX  
PA (ENZO-) ENZON INC.  
XX  
PI Filpula DR, Whitlow MD;  
XX  
WPI: 2000-022812/02.  
DR P-PSDB; AAY54837.  
XX  
XX  
XX Peptide linkers, linked fusion polypeptides containing the linkers and  
XX their preparation -  
XX  
XX Example; Fig 13; 42pp; English.  
XX  
CC This sequence encodes a linked fusion protein containing the  
CC amino acid linker of the invention. The linkers are used for connecting  
CC constituent polypeptides to form novel linked fusion polypeptides.  
CC Polypeptides derived from any protein can be connected, in particular  
CC multichain protein or protein complexes e.g. enzymes, members of the  
CC immunoglobulin superfamily, hormones, DNA-binding proteins. The linker  
CC provides fusion proteins which have greater stability and are less  
CC susceptible to aggregation.

XX  
SQ Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 83.6%; Score 293.6; DB 21; Length 733;  
Best Local Similarity 90.2%; Pred. No. 6.6e-78;  
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCGAGCTGGTGGAGCTCTGGGGAGGCTTAGTGAAGCCTGGAGCTCCCTGAGACTC 60  
Db 376 gaagtgaagctctgaggagctctggggagggcttagtgaagcctggagggtccctgaaactc 435  
QY 61 TCCGTGTCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTGTGGTTTCGCCAGATT 120  
Db 436 tccgtgcagcctctggatctgctttcagtagcctatgacatgtctgggttcgccagact 495  
QY 121 CCGAGAGAGGCTGGAGTGGGTGCAGAAAGTTAGTAGTGTGGTGGTAGCACTACTAT 180  
Db 496 ccgagagaagggctggagtggtgcgaaccattagtagtggtgtagttacacctactat 555  
QY 181 TTAGACACTGTGTCAGGCGCGATTTCACCATCTCCAGAGACAATGCCAAGAACACCTATAC 240  
Db 556 ttagacagtgtgaagggccgattcaccatctccagagacagtgccagaaacacctatac 615  
QY 241 CTGCAATGAGCACTCTGAACCTCTGAGACACAGCCATGTATTACTGTGCAAGACATAAC 300  
Db 616 ctgcaaatgacagctctgaggtctgagacacgacctgtattactgtgcaccgactacg 675  
QY 301 TACGGCAGTTTGTCTTACTGGGGCCAGGGACTCTGGTCACTGTCTCT 348  
Db 676 gtatgccgtttgtctactgggcccaggagactctgtgtcactgtctct 723

RESULT 11  
AAV07642  
ID AAV07642 standard; DNA; 369 BP.  
XX  
AC AAV07642;  
XX  
DT 10-DEC-1998 (first entry)  
XX  
DE anti-CD22 monoclonal antibody heavy chain variable region DNA sequence.  
XX  
KW anti-CD22 monoclonal antibody heavy chain variable region; VL;  
KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;  
KW malignant B-cell; immunodiagnosis; RFB4 IgG; SS.  
XX  
OS Mammalia.  
XX  
FH Key  
FT CDS  
FT /\*tag= a  
FT /transl\_except= (pos:361..363, aa:Thr)  
FT /note= "CDS does not contain a stop codon"  
XX  
PN WO9841641-A1.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US05453.  
XX  
PR 20-MAR-1997; 97US-0041437.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Fitzgerald D, Kreitman R, Mansfield E, Pastan I;  
XX  
WPI: 1998-521227/44.  
DR P-PSDB; AAW66099.  
XX  
XX Recombinant anti-CD22 antibodies and immuno-conjugates - of  
XX antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin  
XX or a label; for inhibiting malignant B-cells

Claim 15; Fig 1; 71pp; English.  
 The present sequence represents the anti-CD22 monoclonal antibody (RFB4 IgG) heavy chain variable region DNA sequence. The invention claims for a recombinant immunoconjugate comprising of a therapeutic agent (e.g Pseudomonas exotoxin) or a detectable label, peptide bonded to a recombinant anti-CD22 antibody having a variable heavy (VH; AA660699) chain with a cysteine residue at amino acid 44 and a variable light (VL; AA660698) chain with a cysteine residue at amino acid 100. The immunoconjugate is claimed to inhibit the growth of malignant B-cells in vivo, such as rodent, canine or primate B-cells. The anti-CD22 antibody is claimed useful for detecting CD22 protein in a sample or in vivo in a mammal, and can be used in diagnostic kits.

Sequence 369 BP; 83 A; 85 C; 110 G; 91 T; 0 other;

```

Query Match          82.98; Score 291; DB 19; Length 369;
Best Local Similarity 89.7%; Pred. No. 3.2e-77;
Matches 331; Conservative 0; Mismatches 20; Indels 18; Gaps 1;

QY 1 GAAGTCAGCTGTGTGGAGTCTGTGGGGAGGCTTACTGAAGCCTGGAAGTCCCTCGAGACTC 60
DB 1 gaagtgcagctgtgtgagctctgtggggagccttagtggaagcctggagggtccctgaaactc 60

QY 61 TCCTGTGCAGCCTCTGATTCGCTTTTCAGTAGCTATGACATGCTCTGGGTTGCGCAGATT 120
DB 61 tcctgtgcagcctctgattcgcttgcagtcattcatgacatgtgttggttgcgcagact 120

QY 121 CCGGAGAAGAGGCTGTGGAGTGGTGCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180
DB 121 ccggagaagagcctgtgagtgagtgagtcgcatactattagtgagtggtgtaccactactat 180

QY 181 TTGACACTGTGCAGGCCGAGTTCCACATCTCCAGAGACAAATGCCAGAACACCCCTATAC 240
DB 181 ccgagacactgtgaaggccgaggtattccaccatctccagagacaaatgccagaaacacctgtac 240

QY 241 CTGCAAAATGAGCAGCTCTGAACCTCTGAGGACACAGCCATGTATTACTGTGCAAGACATAC 300
DB 241 ctgcaaatgagcagctctgaagctctgaagacacagccatgtattactgtgcaagacatagt 300

QY 301 TACGGCAGT-----TTTGCTTACTGGGGCCAGGGACTCTCTGGTCACT 342
DB 301 ggtcacggtagtagctacggggtttgttgcttactggggccagggaactctgtgctcact 360

QY 343 GTCTCTGCA 351
DB 361 gtctctgca 369
  
```

RESULT 12  
 AAV58929  
 ID AAV58929 standard; DNA; 1938 BP.  
 XX  
 AC AAV58929;  
 XX  
 XX 02-FEB-1999 (first entry)  
 XX  
 XX A33 chimeric receptor DNA.  
 DE  
 XX  
 XX Chimeric receptor; A33; colorectal cancer; antigen; tumour;  
 KW cytotoxicity; gene therapy; signal transduction; monoclonal antibody;  
 KW mouse; ss.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 7..1938  
 FT /tag= a  
 XX  
 PN WO9841613-A1.

XX	24-SEP-1998.	
PD		
XX		
XX	13-MAR-1998;	98WO-US03797.
PF		
XX		
XX	14-MAR-1997;	97US-0815030.
PR		
XX	(CASE/) CASENTINI-BOROCZ D.	
PA	(FINE/) FINER M H.	
PA	(GREE/) GREENBURG G B.	
PA	(OTTE/) OTTEN G R.	
XX		
XX	Casentini-Borocz D, Finer MH, Greenburg GB, Otten GR;	
PI		
XX	WPI: 1998-521211/44.	
DR	P-PSDB; AAW73048.	
DR		
XX		
XX	New chimeric DNA encoding membrane-bound receptor for non-MHC	
PT	restricted signal activation - inducing cytotoxic effector cells or	
PT	cytokine production in presence of tumour cells expressing the A33	
PT	antigen, and related vectors	
XX		
XX	Example 3; Page 42-43; 90pp; English.	
PS		
XX		
XX	This DNA sequence codes for murine A33 chimeric receptor (see	
CC	AAW73048) comprising a signal peptide from the V $\kappa$ appa chain of human	
CC	antibody 98-6, light chain and heavy chain variable regions of	
CC	anti-colon cancer antigen A33 murine monoclonal antibody A33, human	
CC	IgG2 constant domain and M1 segment, human CD4 transmembrane domain	
CC	and an intracellular portion of human TCR-associated zeta chain. A	
CC	humanised version of the A33 chimeric receptor has been constructed	
CC	(see AAW73049). Novel chimeric proteins, and DNA encoding them, are	
CC	provided, in which the chimeric proteins are characterised by an	
CC	extracellular domain capable of binding to A33 in a non-MHC	
CC	restricted manner, a transmembrane domain and a cytoplasmic domain	
CC	capable of activating a signalling pathway. Binding of A33 to the	
CC	extracellular domain results in transduction of a signal and	
CC	activation of a signalling pathway in the cell, such that the cell	
CC	may be induced to carry out various functions relating to the	
CC	signalling pathway. The chimeric DNA may be used to modify	
CC	lymphocytes as well as haematopoietic stem cells as precursors	
CC	to a number of important cell types. The modified cells can be	
CC	transplanted (especially as a bone marrow transplant) into a mammal	
CC	to provide a source of cytotoxic effector cells that can kill cells	
CC	expressing the tumour-associated A33 antigen and cytokine producing	
CC	cells. The modified cells are activated in presence of A33+ cells.	
CC	Expression constructs and retrovirus vectors are provided.	
XX		
XX	Sequence 1938 BP: 464 A: 543 C: 557 G: 374 T: 0 other;	

Query Match	82.5%	Score	289.6	DB 19	Length	1938			
Best Local Similarity	90.1%	Pred. No.	1.4e-76						
Matches	310	Conservative	0	Mismatches	34	Indels	0	Gaps	0
QY	1	GAAGTCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGAGGTCCCTCAGACTC	60						
Db	448	gaagtgaagcttggtagctggggagggcttagtgaagcctggaggtccctgaaactc	507						
QY	61	TCCGTGTGAGCCTCTGGATTCGCCTTCAGTAGCTATGACATGCTGTGGTGGTTCGGCCAGATT	120						
Db	508	tccgtgcagcctctggattgcttccagtacctatgacatgcttgggttcgccaact	567						
QY	121	CCGAGAGAGGCTGGAGTGGGTGC AAAATTAGTAGTGGTGGTAGCACCCTACTAT	180						
Db	568	ccggagaagagctggagtggtgcgaacctatgtagtggtggttagttacacctactat	627						
QY	181	TTAGACACTGTGCAGGCGCGATTCCACTATCCAGAGACAATGCCAAGAACACCCCTATAC	240						
Db	628	ttagacagtgtagaaggccgattcaccatcccccgagacagtgccaggacacccctatcac	687						
QY	241	CTGCAAAATGAGCACTCTGAATCTGTAGGACACACGCCCATGTATTACTGTGCAAGACATAAC	300						



Db 688 ctgcaaatgagcagctgtgaggtctgagacacgacctgttattactgtgaccgactacg 747  
 QY 301 TACGGCAGTTTGTCTTACTGGGGCCAAAGGACTCTGTGCTACTGT 344  
 Db 748 gtagtcccgcttcttacttggggccaaaggactctggtcactgt 791

RESULT 13  
 AAQ62764  
 ID AAQ62764 standard; cDNA; 418 BP.  
 AC AAQ62764;  
 XX  
 DT 24-JAN-1995 (first entry)  
 DE Murine KC-4 immunoglobulin heavy chain variable region cDNA.  
 KW Immunoglobulin variable domain; primer: polymerase chain reaction;  
 KW chimeric antibody; human milk fat globule; human breast carcinoma;  
 KW murine anti-human carcinoma monoclonal antibody KC-4; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..417  
 FT /\*tag= a  
 FT /note= "KC-4 VH chain (no termination codon)"  
 FT mat\_peptide 58..417  
 FT /\*tag= b  
 FT /product= heavy\_chain\_V-region  
 FT  
 XX WO9411508-A.  
 XX  
 XX 26-MAY-1994.  
 XX  
 XX 15-NOV-1993; 93WO-US11316.  
 XX  
 XX 13-NOV-1992; 92US-0977706.  
 XX 13-NOV-1992; 92US-0977707.  
 XX 28-SEP-1993; 93US-0128015.  
 XX  
 XX (CANC-) CANCER RES FUND CONTRA COSTA.  
 XX  
 XX WPI; 1994-183509/22.  
 DR P-PSDB; AAR52773.  
 XX  
 XX Chimeric human-murine polypeptide(s) specific for human mammary  
 PT fat globule antigen - for imaging, diagnosing and treating  
 PT neoplasia, with less undesirable immunogenic response  
 XX  
 XX Example 26; Page 40; 54pp; English.  
 CC An initial isolation of cDNAs coding for murine anti-human breast  
 CC carcinoma MAB KC-4 was performed using PCR with commercially  
 CC available primers (see AAQ62751-Q62758, available from NOVAGEN).  
 CC Subsequent cloning using PCR primers JO20, JO21, JO22 and JO24  
 CC (see AAQ62759-Q62762) resulted in the isolation of the mouse Ig  
 CC variable domains. The amplified cDNAs were sequenced (AAQ62763 and  
 CC AAQ62764). Chimeric mouse-human antibodies were constructed  
 CC using human constant regions so as to produce less immunogenic  
 CC polypeptides which retained the anti-human carcinoma binding  
 CC specificity of KC-4.  
 XX  
 XX Sequence 418 BP; 88 A; 94 C; 126 G; 110 T; 0 other;

Query Match 80.9%; Score 284; DB 15; Length 418;  
 Best Local Similarity 89.2%; Pred. No. 4e-75;  
 Matches 321; Conservative 0; Mismatches 30; Indels 9; Gaps 1;

QY 1 GAAGTCAGCTGGTGGAGCTGGGGAGGCTTACTGAAGCTTGGAAAGTCCCTGAGACTC 60  
 Db 58 gaagtcagatggtggagctgtggggaggtcttagtgagcgtgaggtccctgaaactc 117

QY 61 TCCTGTGAGCCTCTGGATTGCTTTTTCAGTACCTATGACATGCTTGGGTTCGCAGATT 120  
 Db 118 tctgtgcagcctctggattcgctttcagtagctatgccatgtcttgggttcgcagctct 177  
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGTGGTGTAGCACCCTACTAT 180  
 Db 178 ccagagaagagctggagtggtgcagaaattagtagtggtggttaattacgcctactat 237  
 QY 181 TTAGACACTGTGACAGGGCCGATTTCACCATCTCCAGAGACATGCCAAGAACCCCTATAC 240  
 Db 238 caagacactgtgacgggcccattccaccatctccagagacaatgccagaacaccctgtac 297  
 QY 241 CTGCAATGAGCAGCTCTGAACCTCTGAGACACAGCCCATGTATTACTGTGCAAGACATAAC 300  
 Db 298 ctggaatgagcagctctgaggtctgagacacggccatgtattactgtgcaaggaggac 357  
 QY 301 TACGG-----CAGTTTGTCTTACTGGGGCCAAAGGACTCTGGTGTGCTCTGTGCA 351  
 Db 358 tacggtatcccgccctggtttgttactgtggggccaaaggactctgtctgtctctgca 417

RESULT 14  
 AAQ62789  
 ID AAQ62789 standard; cDNA; 418 BP.  
 AC AAQ62789;  
 XX  
 DT 24-JAN-1995 (first entry)  
 DE Murine KC-4 immunoglobulin heavy chain variable region cDNA.  
 KW Immunoglobulin variable domain; primer: polymerase chain reaction;  
 KW chimeric antibody; human milk fat globule; human breast carcinoma;  
 KW murine anti-human carcinoma monoclonal antibody KC-4; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..417  
 FT /\*tag= a  
 FT /note= "KC-4 VH chain (no termination codon)"  
 FT mat\_peptide 58..417  
 FT /\*tag= b  
 FT /product= heavy\_chain\_V-region  
 FT  
 XX WO9411509-A.  
 XX  
 XX 26-MAY-1994.  
 XX  
 XX 16-NOV-1993; 93WO-US11445.  
 XX  
 XX 16-NOV-1992; 92US-0977696.  
 XX 30-SEP-1993; 93US-0129930.  
 XX 08-OCT-1993; 93US-0134346.  
 XX  
 XX (CANC-) CANCER RES FUND CONTRA COSTA.  
 XX  
 XX Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;  
 XX WPI; 1994-183510/22.  
 XX  
 XX New analogue peptide(s) comprising antibody variable regions -  
 PT used to develop prods. for use in the detection, diagnosis,  
 PT therapy and prevention of neoplasms  
 XX  
 XX Example 25; Page 60; 109pp; English.  
 PS An initial isolation of cDNAs coding for murine anti-human breast  
 CC carcinoma MAB KC-4 was performed using PCR with commercially  
 CC available primers (see AAQ62776-Q62783, available from NOVAGEN).  
 CC Subsequent cloning using PCR primers JO20, JO21, JO22 and JO24  
 CC (see AAQ62784-Q62787) resulted in the isolation of the mouse Ig

CC variable domains. The amplified cDNAs were sequenced (AA062788 and  
 CC AA062789). Chimeric mouse-human antibodies were constructed  
 CC using human constant regions so as to produce less immunogenic  
 CC polypeptides which retained the anti-human carcinoma binding  
 CC specificity of KC-4.  
 XX  
 SQ Sequence 418 BP; 88 A; 94 C; 136 G; 110 T; 0 other;

Query Match 80.9%; Score 284; DB 15; Length 418;  
 Best Local Similarity 89.2%; Pred. No. 4e-75;  
 Matches 321; Conservative 0; Mismatches 30; Indels 9; Gaps 1;

QY 1 GAAGTGCAGCTGGTGGAGCTGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAGACTC 60  
 DB 58 gaagtgcagctggtagagctctggggagagcttagtgaagcctggagggctccctgaaactc 117  
 QY 61 TCCTGTGAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTTTGGGTTCCGCCAGATT 120  
 DB 118 tcctgtgagcctctggattcgcttttcagtagctatgccatgtcttgggttcgagctct 177  
 QY 121 CCGGAGAAGAGCTGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180  
 DB 178 ccagagaagagctgagtgagtggttcgcagaataatgagcagtggttgaatcacgcctactat 237  
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240  
 DB 238 caagacactgtgacgggagcttaccatctccagagacaatgccaaagacaccctgtac 297  
 QY 241 CTGCAATGAGAGCTGTGACTGTGAGGACAGACAGCCATGTTACTGTGCAAGACATAAC 300  
 DB 298 ctggaataagcagctgagtggttcgagacagcagcagctgattactgtgcaaggaggac 357  
 QY 301 TAGCGG-----CAGTTTGTCTACTGGGCGCAAGGACTGTGCTACTGTCTCTGCA 351  
 DB 358 tacggtatccccggcctggtttgcttactggggcccaaggagactctggctctctctgca 417

RESULT 15  
 AAV24232  
 ID AAV24232 standard; cDNA to mRNA; 411 BP.  
 XX  
 AC AAV24232;  
 XX  
 DT 03-SEP-1998 (first entry)  
 XX  
 DE Chimeric antibody against hTPRP H chain V region cDNA SEQ ID NO:57.  
 XX  
 KW Chimeric; antibody; human parathormone related peptide; hTPRP; mouse;  
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;  
 KW hypophosphemia; pathogen; vitamin D resistance; V region; C region;  
 KW humanised; ds.  
 XX  
 OS Synthetic.  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.

Key Location/Qualifiers  
 FH 1..411  
 FT CDS /tag= a  
 FT /note= "no stop codon given"  
 FT sig\_peptide 1..57  
 FT mat\_peptide /tag= b  
 FT 58..411  
 FT /tag= c  
 XX  
 PN WO9813388-A1.  
 XX  
 PD 02-APR-1998.  
 XX  
 PF 24-SEP-1997; 97WO-JP03382.  
 XX  
 PF 24-JUL-1997; 97JP-0214168.  
 PR

PR 26-SEP-1996; 96JP-0255196.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Sato K, Wakahara Y, Yabuta N;  
 PI  
 XX WPI; 1998-230640/20.  
 DR P-PSDB; AAW57592.  
 XX  
 PT New chimeric antibodies against human parathormone related  
 PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other  
 PT disorders caused by malignant neoplasm(s)  
 XX  
 PS Claim 52; Page 120-121; 182pp; Japanese.  
 XX  
 CC New antibodies have been developed which are specific for human  
 CC parathormone related peptides (hTPRP). The antibodies comprise chimeric  
 CC L and/or H chains, where the C region is of human and L region of mouse,  
 CC origin. The present sequence encodes a specifically claimed region of  
 CC an antibody of the invention. Host cells, transformed with vectors  
 CC containing DNA encoding antibodies of the invention, can be used to  
 CC produce the antibodies. The antibodies may be used to treat  
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of  
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,  
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They  
 CC may also be used for treatment of hypophosphemia such as that due to  
 CC pathogens or to vitamin D resistance.  
 XX  
 SQ Sequence 411 BP; 98 A; 97 C; 109 G; 107 T; 0 other;

Query Match 80.8%; Score 283.6; DB 19; Length 411;  
 Best Local Similarity 89.5%; Pred. No. 5.2e-75;  
 Matches 317; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 1 GAAGTGCAGCTGGTGGAGCTGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAGACTC 60  
 DB 58 gaggtgcaactggtgagctgctggggagagacttagtgaagcctggagggctccctgaaactc 117  
 QY 61 TCCTGTGAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTTTGGGTTCCGCCAGATT 120  
 DB 118 tcctgtgagcctctggattcagcttccagtagctatgcatgtcttggattgcagact 177  
 QY 121 CCGGAGAAGAGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTAT 180  
 DB 178 ccagacaagagctgagtggttcgcacaaccattagtagtggtggttagctacactactat 237  
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240  
 DB 238 ccagacagctgtgaaaggggcgattccaccatctccagagacaatgccaaagacaccctctac 297  
 QY 241 CTGCAATGAGAGCTGTGAACTCTGAGGACACAGCCATGTTACTGTGCAAGACATAAC 300  
 DB 298 ctgcaaatgagcagctgaaagtctgagacacagcagcagcttttactgtgcaagacagact 357  
 QY 301 TAGCGCAGT---TTTGGCTTACTGGGCGCAAGGACTGTGCTACTGTCTCTGCA 351  
 DB 358 actatgacttacttcttactggttactggggcccaaggagactctggtcactgtctctgca 411

Search completed: October 11, 2001, 15:12:37  
 Job time: 6469 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:14:14 ; Search time 87.94 seconds  
(without alignments)  
755.608 Million cell updates/sec

Title: US-08-791-391A-5  
Perfect score: 351  
Sequence: 1 GAAGTGCAGCTGGTGGATC.....CTCTGCTACTGCTCTCTGCA 351

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCRUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	84.0	413	1	US-08-253-877C-56
2	295	84.0	413	2	US-08-452-164A-56
3	293.6	83.6	721	2	US-08-224-591-15
4	293.6	83.6	721	2	US-08-926-789-15
5	293.6	83.6	733	2	US-08-224-591-17
6	293.6	83.6	733	2	US-08-926-789-17
7	284	80.9	418	1	US-07-977-696C-27
8	284	80.9	418	1	US-08-129-930B-27
9	279	79.5	354	4	US-08-487-761-14
10	271	77.2	445	1	US-08-053-171-10
11	271	77.2	491	1	US-08-053-171-6
12	269.4	76.8	923	5	PCT-US94-07659-1
13	267.8	76.3	357	2	US-08-475-000-15
14	267.8	76.3	357	2	US-08-483-199-15
15	267.8	76.3	357	2	US-08-484-508-15
16	266.2	75.8	357	1	US-08-331-398A-21
17	266.2	75.8	357	2	US-08-859-649-26
18	266.2	75.8	357	2	US-08-331-397B-21
19	266.2	75.8	357	2	US-08-759-804A-21
20	266.2	75.8	375	1	US-08-331-398A-59
21	266.2	75.8	375	2	US-08-331-397B-59
22	266.2	75.8	375	2	US-08-759-804A-58
23	264.6	75.4	357	1	US-08-285-936-1
24	264.6	75.4	357	1	US-08-487-860-1
25	263	74.9	357	1	US-08-285-936-5
26	263	74.9	357	1	US-08-487-860-5

28	263	74.9	357	1	US-08-487-860-7
29	263	74.9	357	2	US-08-553-497A-17
30	262.2	74.7	357	1	US-08-207-996-26
31	262.2	74.7	357	2	US-08-760-840A-26
32	262.2	74.7	357	2	US-08-760-840A-27
33	262.2	74.7	357	3	US-09-266-119-26
34	262.2	74.7	357	3	US-09-266-119-27
35	262	74.6	357	3	US-07-956-399-3
36	261.4	74.5	357	1	US-08-285-936-11
37	261.4	74.5	357	1	US-08-487-860-11
38	259.8	74.0	357	1	US-08-487-860-56
39	259.8	74.0	405	4	US-08-579-378A-15
40	259.6	74.0	417	1	US-08-398-613A-21
41	259.6	74.0	417	1	US-08-398-612A-21
42	259.6	74.0	417	1	US-08-398-611A-21
43	259.6	74.0	417	1	US-08-396-851A-21
44	259.6	74.0	417	2	US-08-491-334A-21
45	259.6	74.0	417	3	US-09-027-449-18

ALIGNMENTS

RESULT 1  
US-08-253-877C-56  
; Sequence 56, Application US/08253877C  
; Patent No. 5773001  
; GENERAL INFORMATION:  
; APPLICANT: Hamann, Phillip R.  
; APPLICANT: Himman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Kwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,877C  
; FILING DATE: 03-JUN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 32,368  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3246  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 413 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 6..413  
US-08-253-877C-56

```

Query Match      84.08; Score 295; DB 1; Length 413;
Best Local Similarity 90.08; Pred. No. 9,7e-85;
Matches 316; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGGTGGAGTCTGGGGGAGGCTTACTGAAGCCTGGAAGGTCCTCGAGACTC 60
   |||||
Db 63 GAAGTGAAGCTGGTGGAGTCTGGGGGAGGCTTACTGAAGCCTGGAAGGTCCTCGAAACTC 122
   |||||

QY 61 TCCTGTCCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGATT 120
   |||||
Db 123 TCCTGTCCAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGTCTTGGGTTTCGCCAGACT 182
   |||||

QY 121 CCGGAGAAGAGGCTGGAGTGGGTGGCGCAAAAGTTAGTAGTGGTGGTGGTAGCACCCTACTAT 180
   |||||
Db 183 CCGGAGAAGAGGCTGGAGTGGGTGGCGCAACCACTTAGTAGTGGTGGTGGTAGTACACTACTAT 242
   |||||

QY 181 TTAGACACTGTGCAGGCGCGATTCACCATCTCCAGAGACAATGCCAGAGACACCCCTATAC 240
   |||||
Db 243 TTAGACACTGTGAAGGCGCGATTCACCATCTCCAGAGACAGTCCCGAGAACACCCCTATAC 302
   |||||

QY 241 CTGCAATGAGCAGCTCGAACTCTGAGGACACACGCCATGTATTACTGTGCAAGACATAAC 300
   |||||
Db 303 CTGCAATGAGCAGCTCGAGCTCTGAGGACACGCCCTGTATTACTGTGCAAGCAGTACG 362
   |||||

QY 301 TACGGCAGTTTGTCTTACTGGGGCCAAAGGAGCTCTGGTCACTGTCTCTGCA 351
   |||||
Db 363 GTAGTCCCGTTGTCTTACTGGGGCCAAAGGAGCTCTGGTCACTGTCTCTGCA 413
   |||||

RESULT 2
US-08-452-164A-56
; Sequence 56, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyllirithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 721 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..711)  
US-08-224-591-15

Query Match 83.6%; Score 293.6; DB 2; Length 721;  
Best Local Similarity 90.2%; Pred. No. 3.3e-84;  
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTGCAGCTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60  
DB 364 GAAGTGAAGCTTGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAAACTC 423  
QY 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 120  
DB 424 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGACT 483  
QY 121 CCGGAGAAGAGCCTGGAGTGGGTGCGAAAGCTTAGTAGTGGTGGTAGCACCTACTAT 180  
DB 484 CCGGAGAAGAGCCTGGAGTGGGTGCGCAACCATTAGTAGTGGTGGTAGCACCTACTAT 543  
QY 181 TTAGACACTGTGAGGCGCGATTCCACCATCTCCAGAGACAAATGCGCAAGACACCTATAC 240  
DB 544 TTAGACACTGTGAGGCGCGATTCCACCATCTCCAGAGACAGTGGCCAGAACACCTATAC 603  
QY 241 CTGCAATGACAGCTGCACTCTGAGGACAGCAGCCATGATGCTGTCAGGAGACTAC 300  
DB 604 CTGCAATGACAGCTGCACTCTGAGGACAGCAGCCATGATGCTGTCAGGAGACTAC 663  
QY 301 TACGGCAGTTTGTCTTACTGGGGCCAGGAGCTCTGGTCACTGTCTCT 348  
DB 664 GTAGTCCCGTTTGTCTTACTGGGGCCAGGAGCTCTGGTCACTGTCTCT 711

RESULT 4  
US-08-926-789-15  
; Sequence 15, Application US/08926789  
; Patent No. 5990275  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/926,789  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/224,591  
; FILING DATE:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 721 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: join(1..711)  
US-08-926-789-15

Query Match 83.6%; Score 293.6; DB 2; Length 721;  
Best Local Similarity 90.2%; Pred. No. 3.3e-84;  
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTGCAGCTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60  
DB 364 GAAGTGAAGCTTGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAAACTC 423  
QY 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGATT 120  
DB 424 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGCTATGACATGCTTGGGTTGCCAGACT 483  
QY 121 CCGGAGAAGAGCCTGGAGTGGGTGCGAAAGCTTAGTAGTGGTGGTAGCACCTACTAT 180  
DB 484 CCGGAGAAGAGCCTGGAGTGGGTGCGCAACCATTAGTAGTGGTGGTAGCACCTACTAT 543  
QY 181 TTAGACACTGTGAGGCGCGATTCCACCATCTCCAGAGACAAATGCGCAAGACACCTATAC 240  
DB 544 TTAGACACTGTGAGGCGCGATTCCACCATCTCCAGAGACAGTGGCCAGAACACCTATAC 603  
QY 241 CTGCAATGACAGCTGCACTCTGAGGACAGCAGCCATGATGCTGTCAGGAGACTAC 300  
DB 604 CTGCAATGACAGCTGCACTCTGAGGACAGCAGCCATGATGCTGTCAGGAGACTAC 663  
QY 301 TACGGCAGTTTGTCTTACTGGGGCCAGGAGCTCTGGTCACTGTCTCT 348  
DB 664 GTAGTCCCGTTTGTCTTACTGGGGCCAGGAGCTCTGGTCACTGTCTCT 711

RESULT 5  
US-08-224-591-17  
; Sequence 17, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,591

;; FILING DATE: Herewith  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/002,845  
;; FILING DATE: 15-JAN-1993  
;; APPLICATION NUMBER: US 07/980,529  
;; FILING DATE: 20-NOV-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 733 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: join(1..723)  
US-08-224-591-17

Query Match 83.6%; Score 293.6; DB 2; Length 733;  
Best Local Similarity 90.2%; Pred. No. 3.4e-84;  
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGGTGGAGCTGTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60  
DB 376 GAAGTGAAGCTTGTGGAGCTGTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAAACTC 435

QY 61 TCCTGTGACGCTCTGGATTCGTTTCAGTAGCTATGACATGTTCTGGGTTCGCCAGATT 120  
DB 436 TCCTGTGACGCTCTGGATTCGTTTCAGTAGCTATGACATGTTCTGGGTTCGCCAGATT 495

QY 121 CCGGAGAAGAGGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCCTACTAT 180  
DB 496 CCGGAGAAGAGGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCCTACTAT 555

QY 181 TTAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 240  
DB 556 TTAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 615

QY 241 CTCGAAATGAGCAGCTGAACTCTGAGGACAGCCATGTTACTGTGCAAGACATAAC 300  
DB 616 CTCGAAATGAGCAGCTGAACTCTGAGGACAGCCATGTTACTGTGCAAGCAGTACG 675

QY 301 TAGCGCAGTTTGTCTTACTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 348  
DB 676 GTAGTCCCGTTTGTCTTACTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 723

RESULT 6  
US-08-926-789-17  
; Sequence 17, Application US/08926789  
; Patent No. 5990275  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/926,789  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/224,591  
;; FILING DATE:  
;; APPLICATION NUMBER: US 08/002,845  
;; FILING DATE: 15-JAN-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/980,529  
;; FILING DATE: 20-NOV-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 733 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: join(1..723)  
US-08-926-789-17

Query Match 83.6%; Score 293.6; DB 2; Length 733;  
Best Local Similarity 90.2%; Pred. No. 3.4e-84;  
Matches 314; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAAGTCAGCTGGTGGAGCTGTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAGACTC 60  
DB 376 GAAGTGAAGCTTGTGGAGCTGTGGGGAGGCTTAGTGAAGCCTGGAAGTCCCTGAAACTC 435

QY 61 TCCTGTGACGCTCTGGATTCGTTTCAGTAGCTATGACATGTTCTGGGTTCGCCAGATT 120  
DB 436 TCCTGTGACGCTCTGGATTCGTTTCAGTAGCTATGACATGTTCTGGGTTCGCCAGATT 495

QY 121 CCGGAGAAGAGGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCCTACTAT 180  
DB 496 CCGGAGAAGAGGCTGGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCCTACTAT 555

QY 181 TTAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 240  
DB 556 TTAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 615

QY 241 CTCGAAATGAGCAGCTGAACTCTGAGGACAGCCATGTTACTGTGCAAGACATAAC 300  
DB 616 CTCGAAATGAGCAGCTGAACTCTGAGGACAGCCCTTGTATTACTGTGCAAGCAGTACG 675

QY 301 TAGCGCAGTTTGTCTTACTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 348  
DB 676 GTAGTCCCGTTTGTCTTACTGGGCGCAAGGAGCTCTGGTCACTGTCTCT 723

RESULT 7  
US-07-977-696C-27  
; Sequence 27, Application US/07977696C  
; Patent No. 5792852  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity



;; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
;; TITLE OF INVENTION: and Therapeutic Methods.  
;; NUMBER OF SEQUENCES: 81  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
;; STREET: 444 South Flower Street, Suite 2000  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90071  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/977,696C  
;; FILING DATE: 11-16-92  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Amzel Ph.D., Viviana  
;; REGISTRATION NUMBER: 30,930  
;; REFERENCE/DOCKET NUMBER: P66 38227  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (510) 748-6868  
;; TELEFAX: (510) 748-6688  
;; TELEX: n.a.  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 418 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-07-977-696C-27

Query Match 80.9%; Score 284; DB 1; Length 418;  
Best Local Similarity 89.2%; Pred. No. 3e-81;  
Matches 321; Conservative 0; Mismatches 30; Indels 9; Gaps 1;

Qy 1 GAAGTGCAGCTGGGAGCTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCGAGACTC 60  
Db 58 GAAGTGCAGATGGTGGAGCTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCGAAACTC 117  
Qy 61 TCCTGTGCAGCCTCTGGATTGCTTTCAGTAGCTATGACATCTCTTGGGTTGCCAGATT 120  
Db 118 TCCTGTGCAGCCTCTGGATTGCTTTCAGTAGCTATGACATCTCTTGGGTTGCCAGATT 177  
Qy 121 CCGGAGAAGAGGCTGGAGTGGTTCGCAAAAGTTAGTGTGGTGGTAGCACCTTACTAT 180  
Db 178 CCAGAGAAGAGGCTGGAGTGGTTCGCAAAAGTTAGTGTGGTGGTAGCACCTTACTAT 237  
Qy 181 TTAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 240  
Db 238 CAAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATGCCAAGACACCCCTGTAC 297  
Qy 241 CTGCAAAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTTATTACTGTGCAAGACATAAC 300  
Db 298 CTGGAATGACAGCTCTGAGGCTCTGAGGACACAGCCATGTTATTACTGTGCAAGGAGGAC 357  
Qy 301 TACGG-----CAGTTTGTCTTACTGGGCGCAAGGAGCTCTGGTCTCTCTGCTGCA 351  
Db 358 TACGGTATCCCGGCTGTGTTGCTTACTGGGCGCAAGGAGCTCTGGTCTCTCTGCTGCA 417

RESULT 8  
US-08-129-930B-27  
; Sequence 27, Application US/08129930B  
; Patent No. 5804187  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.

;; APPLICANT: Peterson Dr., Jerry A.  
;; APPLICANT: Padlan Dr., Eduardo A.  
;; TITLE OF INVENTION: Analogue Peptides With Broad  
;; TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
;; TITLE OF INVENTION: Diagnostic Vaccination and  
;; TITLE OF INVENTION: Therapeutic Methods  
;; NUMBER OF SEQUENCES: 96  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: V. AMZEL & ASSOC.  
;; STREET: 2055 No. 5804187th Broadway, Suite 201  
;; CITY: Walnut Creek  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94596  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/129,930B  
;; FILING DATE: September 30, 1993  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Amzel Ph.D., Viviana  
;; REGISTRATION NUMBER: 30,930  
;; REFERENCE/DOCKET NUMBER: CRFCC-008A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (510) 521-1333  
;; TELEFAX: (510) 521-3541  
;; TELEX: n.a.  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 418 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-08-129-930B-27

Query Match 80.9%; Score 284; DB 1; Length 418;  
Best Local Similarity 89.2%; Pred. No. 3e-81;  
Matches 321; Conservative 0; Mismatches 30; Indels 9; Gaps 1;

Qy 1 GAAGTGCAGCTGGTGGAGCTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCGAGACTC 60  
Db 58 GAAGTGCAGATGGTGGAGCTCTGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTCGAAACTC 117  
Qy 61 TCCTGTGCAGCCTCTGGATTGCTTTCAGTAGCTATGACATCTCTTGGTTCGCCAGATT 120  
Db 118 TCCTGTGCAGCCTCTGGATTGCTTTCAGTAGCTATGACATCTCTTGGTTCGCCAGATT 177  
Qy 121 CCGGAGAAGAGGCTGGAGTGGTTCGCAAAAGTTAGTGTGGTGGTAGCACCTTACTAT 180  
Db 178 CCAGAGAAGAGGCTGGAGTGGTTCGCAAAAGTTAGTGTGGTGGTAGCACCTTACTAT 237  
Qy 181 TTAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATGCCAAGACACCCCTATAC 240  
Db 238 CAAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATGCCAAGACACCCCTGTAC 297  
Qy 241 CTGCAAAATGACAGCTCTGAACCTCTGAGGACACAGCCATGTTATTACTGTGCAAGACATAAC 300  
Db 298 CTGGAATGACAGCTCTGAGGCTCTGAGGACACAGCCATGTTATTACTGTGCAAGGAGGAC 357  
Qy 301 TACGG-----CAGTTTGTCTTACTGGGCGCAAGGAGCTCTGGTCTCTCTGCTGCA 351  
Db 358 TACGGTATCCCGGCTGTGTTGCTTACTGGGCGCAAGGAGCTCTGGTCTCTCTGCTGCA 417

RESULT 9  
US-08-487-761-14  
; Sequence 14, Application US/08487761

Patent No. 6217866  
 GENERAL INFORMATION:  
 APPLICANT: Schlusser, Joseph  
 APPLICANT: Givol, David  
 APPLICANT: Bellot, Françoise  
 APPLICANT: Kris, Richard  
 APPLICANT: Ricca, George A.  
 APPLICANT: Cheadle, Christopher  
 APPLICANT: South, Victoria J.  
 TITLE OF INVENTION: Monoclonal Antibodies Specific to Human  
 TITLE OF INVENTION: Epidermal Growth Factor Receptor and Therapeutic Methods  
 NUMBER OF INVENTIONS: 17  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Road, 3C43  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: System 7.1  
 SOFTWARE: Word 5.0 (Patent In)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,761  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/086,411  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goodman, Rosanne  
 REGISTRATION NUMBER: 32,534  
 REFERENCE/DOCKET NUMBER: A0207C-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 454-3817  
 TELEFAX: (215) 454-3808  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 354 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..354  
 US-08-487-761-14

Query Match 79.5%; Score 279; DB 4; Length 354;  
 Best Local Similarity 90.5%; Pred. No. 1.1e-79;  
 Matches 323; Conservative 0; Mismatches 25; Indels 9; Gaps 2;  
 QY 1 GAAGTCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTGAGACTC 60  
 DB 1 GAAGTCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTGGAAGT 60  
 QY 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGTACATGCTTGGGTTCGCCAGATT 120  
 DB 61 TCCTGTGAGCCTCTGGATTCGCTTTCAGTAGTACATGCTTGGGTTCGCCAGACT 120  
 QY 121 CCGGAGAAGAGGCTGGAGTGGGTTCGAAAGTGTAGTGGTGGTGGTGGTGGTGGTGGT 180  
 DB 121 CCGGAGAAGAGGCTGGAGTGGGTTCGAAAGTGTAGTGGTGGTGGTGGTGGTGGTGGT 177  
 QY 181 TTAGACACTGTGCGAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240  
 DB 178 CCAGACACTGTGGAAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 237  
 QY 241 CTGCAANTAGCAGCTGTAAGTCTGAGGACACAGCCATGCTATTACTGTGTCGAAGACA 296

DB 238 CTTCAATGAGCAGTCTGAAGTCTGAGGACACAGCCATTATTACTGTGCAAGTCACTAT 297  
 QY 297 --TAAGTACGGCAGTTTCTGCTTACTGGGCGCAAGGACTCTGGTCACTGTCTGTGCA 351  
 DB 298 GGTACGACGGGAGGTTGCTTACTGGGCGCAAGGACTCTGGTCACTGTCTGTGCA 354  
 RESULT 10  
 US-08-053-171-10  
 ; Sequence 10, Application US/08053171  
 ; Patent No. 5562903  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co, Loibner  
 ; TITLE OF INVENTION: Antibody Derivatives  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Hourie and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/053,171  
 ; FILING DATE: 22-APR-1993  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-54-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 1..445  
 ; OTHER INFORMATION: /standard\_name= "Heavy Chain  
 ; OTHER INFORMATION: V-region of BR55-2 Antibody in pVg-1c and pVg-3c"  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 12..425  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 1..6  
 ; OTHER INFORMATION: /standard\_name= "Xba I restriction  
 ; OTHER INFORMATION: site"  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 440..445  
 ; OTHER INFORMATION: /standard\_name= "Xba I restriction  
 ; OTHER INFORMATION: site"  
 ; US-08-053-171-10

Query Match 77.2%; Score 271; DB 1; Length 445;  
 Best Local Similarity 87.1%; Pred. No. 4.2e-77;  
 Matches 311; Conservative 0; Mismatches 40; Indels 6; Gaps 1;  
 QY 1 GAAGTCAGCTGGTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAAGGTCCTGAGACTC 60



SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 923 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 169..909  
PCT-US94-07659-1

Query Match 76.8%; Score 269.4; DB 5; Length 923;  
Best Local Similarity 86.8%; Pred. No. 1.8e-76;  
Matches 310; Conservative 0; Mismatches 41; Indels 6; Gaps 1;  
QY 1 GAAGTCAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAAGCTCCCTGAGACTC 60  
DB 226 GAAGTCAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAACTC 285  
QY 61 TCCTGTGAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTCTTTGGGTCGCCAGATT 120  
DB 286 TCCTGTGAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTCTTTGGGTCGCCAGACT 345  
QY 121 CCGGAGAGAGGCTGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGGAGCCTACTAT 180  
DB 346 CCGGAGAGAGGCTGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGGAGCCTACTAT 405  
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240  
DB 406 CCAGACACTGTGAAGGCGGATTCACCATCTCCAGGAGACAATGCCAAGAACACCCCTGTAC 465  
QY 241 CTGCAATGAGCAGTCTGAAGTCTGAGGACAGCCATGATTTACTGTGCAAGA----- 294  
DB 466 CTGCAATGAGCAGTCTGAAGTCTGAGGACAGCCATGATTTACTGTGCAAGAGGGGG 525  
QY 295 CATAACTACGGCAGTTTCTGCTTACTGGGCGCAAGGAGCTCTGTCACTCTCTCTGCA 351  
DB 526 GTACGAGAGGGTACTTCGATCTCTGGGGCGGAGGAGCAGGCTACCGCTCTCTCTCA 582

RESULT 13  
US-08-475-000-15  
Sequence 15, Application US/08475000  
Patent No. 5811267  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,000  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..357  
US-08-475-000-15

Query Match 76.3%; Score 267.8; DB 1; Length 357;  
Best Local Similarity 86.6%; Pred. No. 4e-76;  
Matches 309; Conservative 0; Mismatches 42; Indels 6; Gaps 1;  
QY 1 GAAGTCAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAAGTCCCTGAGACTC 60  
DB 1 GAGGTGAAGCTGGTGGAGCTGGGGGAGGCTTAGTGAAGCTGGAGGCTCCCTGAACTC 60  
QY 61 TCCTGTGAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTCTTTGGGTCGCCAGATT 120  
DB 61 TCCTGTGAGCCTCTGGATTCGCTTTTCAGTAGCTATGACATGCTCTTTGGGTCGCCAGACT 120  
QY 121 CCGGAGAGAGGCTGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGGAGCCTACTAT 180  
DB 121 CCGGAGAGAGGCTGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGGAGCCTACTAT 180  
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCCCTATAC 240  
DB 181 CCAGACACTGTGAAGGCTGATTCACCGTCTCCAGAGACAATGCCATGAGAGCCTGTAC 240  
QY 241 CTGCAATGAGCAGTCTGAAGTCTGAGGACAGCCATGATTTACTGTGCAAGACA----- 296  
DB 241 CTGCAATGAGCAGTCTGAAGTCTGAGGACAGCCCTTTGTTACTGTGCAAGATACGGG 300  
QY 297 --TAAGTACGGCAGTTTCTGCTTACTGGGCGCAAGGAGCTCTGTCACTCTCTCTGCA 351  
DB 301 GCTGTGAGCCTGGTTCGCTTACTGGGCGCAAGGAGCTCTGTGTCACAGTTCTTGCA 357

RESULT 14  
US-08-483-199-15  
Sequence 15, Application US/08483199  
Patent No. 5849877  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483.199  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVEREIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..357  
US-08-483-199-15

Query Match 76.3%; Score 267.8; DB 2; Length 357;  
Best Local Similarity 86.6%; Pred. No. 4e-76;  
Matches 309; Conservative 0; Mismatches 42; Indels 6; Gaps 1;  
QY 1 GAAGTGCAGCTGGGGAGCTCTGGGGAGGCTTAGTGAAGCTGGAAGCTCCCTGAGACTC 60  
Db 1 GAGGTGAAGTTGGAGTCTGGGGAGTCTTAGTGAGGCTGGAGGCTCCCTGAAACTC 60  
QY 61 TCCTGTGCAGCTCTGGATTCGCTTTTCAGTAGCTATGACATGTCTTGGGTTCCGCCAGATT 120  
Db 61 TCCTGTGCAGCTCTGGATTCACITTCAGTAGGTATACCATGTCTTGGTTCCGCCAGACT 120  
QY 121 CCGAGAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180  
Db 121 CCGAGAGAGGCTGGAGTGGGTCGCAACCATTTAGTAGTGGTGGTAAACACCTACTAT 180  
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCTATAC 240  
Db 181 CCAGACAGTGTGAAGGTCGATTCACCGTCTCCAGAGACAATGCCATGAGCAGCCTGTAC 240  
QY 241 CTGCAATGAGCAGCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACA---- 296  
Db 241 CTGCAATGAGCAGCTGAGTCTGAGGACACGCGCTTGTATTACTGTGCAAGATACGGG 300  
QY 297 --TAACACGCGAGTTTGGCTTACTGGGGCAAGGGACTCTGGTCACTGTCTCTGCA 351  
Db 301 GCTGGTACGCGCTGGTTGGCTTACTGGGGCAAGGGACTCTGGTCACTGTCTCTGCA 357

RESULT 15  
US-08-484-508-15  
Sequence 15, Application US/08484508  
Patent No. 5948647  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484.508  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVEREIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..357  
US-08-484-508-15

Query Match 76.3%; Score 267.8; DB 2; Length 357;  
Best Local Similarity 86.6%; Pred. No. 4e-76;  
Matches 309; Conservative 0; Mismatches 42; Indels 6; Gaps 1;  
QY 1 GAAGTGCAGCTGGGGAGCTCTGGGGAGGCTTAGTGAAGCTGGAAGCTCCCTGAGACTC 60  
Db 1 GAGGTGAAGTTGGAGTCTGGGGAGTCTTAGTGAGGCTGGAGGCTCCCTGAAACTC 60  
QY 61 TCCTGTGCAGCTCTGGATTCGCTTTTCAGTAGCTATGACATGTCTTGGGTTCCGCCAGATT 120  
Db 61 TCCTGTGCAGCTCTGGATTCACITTCAGTAGGTATACCATGTCTTGGTTCCGCCAGACT 120  
QY 121 CCGAGAGAGGCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTAT 180  
Db 121 CCGAGAGAGGCTGGAGTGGGTCGCAACCATTTAGTAGTGGTGGTAAACACCTACTAT 180  
QY 181 TTAGACACTGTGCAGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACCTATAC 240  
Db 181 CCAGACAGTGTGAAGGTCGATTCACCGTCTCCAGAGACAATGCCATGAGCAGCCTGTAC 240  
QY 241 CTGCAATGAGCAGCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGACA---- 296  
Db 241 CTGCAATGAGCAGCTGAGTCTGAGGACACGCGCTTGTATTACTGTGCAAGATACGGG 300  
QY 297 --TAACACGCGAGTTTGGCTTACTGGGGCAAGGGACTCTGGTCACTGTCTCTGCA 351  
Db 301 GCTGGTACGCGCTGGTTGGCTTACTGGGGCAAGGGACTCTGGTCACTGTCTCTGCA 357

Search completed: October 11, 2001, 15:14:14  
Job time: 5001 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:32 ; Search time 2122.65 Seconds  
(without alignments)  
2339.127 Million cell updates/sec

Title: US-08-791-391A-7  
Perfect score: 321  
Sequence: 1 GATATTGTCTAACTCAGTC.....GGACCAAGCTGGAATTAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_ba3.\*
- 4: gb\_in1.\*
- 5: gb\_in2.\*
- 6: gb\_in3.\*
- 7: gb\_om.\*
- 8: gb\_ov.\*
- 9: gb\_pat1.\*
- 10: gb\_pat2.\*
- 11: gb\_ph.\*
- 12: gb\_pl1.\*
- 13: gb\_pl2.\*
- 14: gb\_pl3.\*
- 15: gb\_pl4.\*
- 16: gb\_ba1.\*
- 17: gb\_ba2.\*
- 18: em\_fun.\*
- 19: em\_htgo\_hum.\*
- 20: em\_htgo\_inv.\*
- 21: em\_htgo\_rod.\*
- 22: em\_htg\_hum1.\*
- 23: em\_htg\_hum2.\*
- 24: em\_htg\_hum3.\*
- 25: em\_htg\_hum4.\*
- 26: em\_htg\_hum5.\*
- 27: em\_htg\_hum6.\*
- 28: em\_htg\_hum7.\*
- 29: em\_htg\_hum8.\*
- 30: em\_htg\_inv1.\*
- 31: em\_htg\_inv2.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_rod.\*
- 34: em\_hum1.\*
- 35: em\_hum2.\*
- 36: em\_hum3.\*
- 37: em\_hum4.\*
- 38: em\_hum5.\*
- 39: em\_hum6.\*
- 40: em\_hum7.\*
- 41: em\_in.\*
- 42: em\_om.\*
- 43: em\_or.\*

- 44: em\_ov.\*
- 45: em\_pat.\*
- 46: em\_ph.\*
- 47: em\_pl.\*
- 48: em\_ro.\*
- 49: em\_sts.\*
- 50: em\_sy.\*
- 51: em\_un.\*
- 52: em\_vi.\*
- 53: gb\_sts1.\*
- 54: gb\_sts2.\*
- 55: gb\_sts3.\*
- 56: gb\_sy.\*
- 57: gb\_un.\*
- 58: gb\_vil.\*
- 59: gb\_vil2.\*
- 60: gb\_htg1.\*
- 61: gb\_htg2.\*
- 62: gb\_htg3.\*
- 63: gb\_htg4.\*
- 64: gb\_htg5.\*
- 65: gb\_htg6.\*
- 66: gb\_htg7.\*
- 67: gb\_htg8.\*
- 68: gb\_htg9.\*
- 69: gb\_htg10.\*
- 70: gb\_htg11.\*
- 71: gb\_htg12.\*
- 72: gb\_htg13.\*
- 73: gb\_htg14.\*
- 74: gb\_htg15.\*
- 75: gb\_htg16.\*
- 76: gb\_htg17.\*
- 77: gb\_htg18.\*
- 78: gb\_htg19.\*
- 79: gb\_htg20.\*
- 80: gb\_htg21.\*
- 81: gb\_htg22.\*
- 82: gb\_htg23.\*
- 83: gb\_htg24.\*
- 84: gb\_htg25.\*
- 85: gb\_pr1.\*
- 86: gb\_pr2.\*
- 87: gb\_pr3.\*
- 88: gb\_pr4.\*
- 89: gb\_pr5.\*
- 90: gb\_pr6.\*
- 91: gb\_pr7.\*
- 92: gb\_pr8.\*
- 93: gb\_pr9.\*
- 94: gb\_rol.\*
- 95: gb\_rol2.\*
- 96: gb\_in4.\*
- 97: gb\_pr10.\*
- 98: em\_ba3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	321	100.0	321	9	AX060786
2	297.6	92.7	321	94	MUSIGKACY
3	296	92.2	321	94	AF163757
4	296	92.2	321	94	MUSCMVH
5	296	92.2	370	94	MUSIGKXD
6	296	92.2	381	10	E07933
7	296	92.2	381	10	I31959
8	296	92.2	381	10	I78571
					AX060786 Sequence
					M35667 Mouse lysoz
					AF163757 Mus muscu
					M95945 Mouse mRNA
					M93959 Mouse Ig ac
					E07933 cDNA encodi
					I31959 Sequence 82
					I78571 Sequence 82

```

9      296      92.2      381 10      I78626
10     296      92.2      431 94      M59913 Sequence 82
11     294.4      91.7      431 94      M59913 Mouse Ig re
12     294.4      91.7      431 94      M59913 Mouse mRNA
13     292.8      91.2      324 94      AF139849 Mus muscu
14     292.8      91.2      324 94      AF139845 Mus muscu
15     291.2      90.7      321 94      AF139846 Mus muscu
16     291.2      90.7      321 94      AF139847 Mus muscu
17     291.2      90.7      321 94      AF139847 Mus muscu
18     291.2      90.7      324 94      AF139847 Mus muscu
19     291.2      90.7      330 94      AF139847 Mus muscu
20     291.2      90.7      381 94      AF139847 Mus muscu
21     291.2      90.7      381 94      AF139847 Mus muscu
22     290.8      90.6      324 94      AF139847 Mus muscu
23     289.6      90.2      321 94      AF139847 Mus muscu
24     289.6      90.2      321 94      AF139847 Mus muscu
25     289.6      90.2      324 94      AF139847 Mus muscu
26     289.6      90.2      348 94      AF139847 Mus muscu
27     289.6      90.2      420 94      AF139847 Mus muscu
28     289.6      90.2      738 94      AF139847 Mus muscu
29     289.6      90.2      5238 94      AF139847 Mus muscu
30     289.6      90.2      5238 94      AF139847 Mus muscu
31     288.8      89.7      582 94      AF139847 Mus muscu
32     286.8      89.3      317 94      AF139847 Mus muscu
33     286.4      89.2      324 94      AF139847 Mus muscu
34     284.8      88.7      381 94      AF139847 Mus muscu
35     283.4      88.3      321 94      AF139847 Mus muscu
36     283.2      88.2      321 94      AF139847 Mus muscu
37     282.4      88.0      323 94      AF139847 Mus muscu
38     282.2      87.9      318 94      AF139847 Mus muscu
39     282.2      87.9      306 94      AF139847 Mus muscu
40     281.6      87.7      300 94      AF139847 Mus muscu
41     281.4      87.7      307 94      AF139847 Mus muscu
42     280.6      87.4      313 94      AF139847 Mus muscu
43     280.4      87.4      315 94      AF139847 Mus muscu
44     280.4      87.2      324 94      AF139847 Mus muscu
45     279.6      87.1      313 94      AF139847 Mus muscu

```

## ALIGNMENTS

```

RESULT 1
AX060786
LOCUS      AX060786      321 bp      DNA
DEFINITION      Sequence 7 from Patent WO0078815.
ACCESSION      AX060786
VERSION      AX060786.1      GI:12406166
KEYWORDS      house mouse.
SOURCE      Mus musculus.
ORGANISM      Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      1. (bases 1 to 321)
JOURNAL      Huse, W.D. and Wu, H.
JOURNAL      Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL      encoding same and methods of use
JOURNAL      Patent: WO 0078815-A 7 28-DEC-2000;
JOURNAL      Applied Molecular Evolution (US)
FEATURES      Location/Qualifiers
source      1..321
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            <!.>.321
            /note="unnamed protein product"
            /codon_start=1
            /protein_id="CAC24891.1"
            /db_xref="GI:12406167"
            /translation="DIVLTQSPATLSVTPGDSVLSQASQISNHLHWYQKSHESP
            RLLIKYASQISIGIPSRFSGSGGDTFALINSVETEDFGMYFCQQSGSWPRTGGGT
            KLEIR"
BASE COUNT*      83 a      83 c      77 g      78 t
ORIGIN

```

```

Query Match      100.0%; Score 321; DB 9; Length 321;
Best Local Similarity      100.0%; Pred. No. 3.8e-99;
Matches 321; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1      GATATTGTGCTAACTACTAGTCTCAGCCACCCCTGTCTGTGTGACACCCAGGAGATAGCGTCAGT 60
Db      1      GATATTGTGCTAACTACTAGTCTCAGCCACCCCTGTCTGTGTGACACCCAGGAGATAGCGTCAGT 60

QY      61      CTTTCTCGCCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTGTATCAACAAAAATCA 120
Db      61      CTTTCTCGCCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTGTATCAACAAAAATCA 120

QY      121      CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGGATCCCTCC 180
Db      121      CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTCCAGTCCATCTCTGGGATCCCTCC 180

QY      181      AGTTCAGTGGCAGTGGATGAGGACAGATTTGGCTCTCAGTATCAACAGTGTGGAGACT 240
Db      181      AGTTCAGTGGCAGTGGATGAGGACAGATTTGGCTCTCAGTATCAACAGTGTGGAGACT 240

QY      241      GAAGATTTTGGATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGS 300
Db      241      GAAGATTTTGGATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGS 300

QY      301      GGGACCAAGCTGGAATTAAG 321
Db      301      GGGACCAAGCTGGAATTAAG 321

RESULT 2
MUSIGKACY      321 bp      mRNA
LOCUS      MUSIGKACY
DEFINITION      Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
ACCESSION      M35667
VERSION      M35667.1      GI:196584
KEYWORDS      immunoglobulin light chain; immunoglobulin-kappa; processed gene;
            variable region VK23.
SOURCE      Mouse hybridoma, cDNA to mRNA, clone 10K-106.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 321)
AUTHORS      Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and
            Brooks, W.B.R.
TITLE      A three-dimensional model of an anti-lysozyme antibody
JOURNAL      J. Mol. Biol. 194, 713-724 (1987)
MEDLINE      88011212
FEATURES      Location/Qualifiers
source      1..321
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            <!.>.321
            /note="lysozyme binding Ig kappa chain V23-J2 region"
            /codon_start=1
            /protein_id="AAA38741.1"
            /db_xref="GI:196585"
            /translation="DIVLTQSPATLSVTPGNSVLSQASQISNHLHWYQKSHESP
            RLLIKYASQISIGIPSRFSGSGGDTFALINSVETEDFGMYFCQQSNWPYRGGGT
            KLEIR"
BASE COUNT      88 a      80 c      75 g      78 t
ORIGIN

```

```

Query Match      92.7%; Score 297.6; DB 94; Length 321;
Best Local Similarity      95.6%; Pred. No. 4.2e-91;
Matches 306; Conservative      0; Mismatches      14; Indels      0; Gaps      0;

QY      1      GATATTGTGCTAACTACTAGTCTCAGCCACCCCTGTCTGTGTGACACCCAGGAGATAGCGTCAGT 60
Db      1      GATATTGTGCTAACTACTAGTCTCAGCCACCCCTGTCTGTGTGACACCCAGGAGATAGCGTCAGT 60

```



```

61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||

RESULT 3
AF163757
LOCUS AF163757 321 bp mRNA ROD 04-AUG-1999
DEFINITION Mus musculus mab 101.4.1 immunoglobulin light chain variable region
ACCESSION AF163757
VERSION AF163757.1 GI:5690320
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 321)
AUTHORS Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal
JOURNAL Mouse Monoclonal Antibodies
REFERENCE 2 (bases 1 to 321)
AUTHORS Mertens, N.M. and Cunningham, M.W.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma
City, OK 73190, USA
FEATURES
source Location/Qualifiers
1..321
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/note="mab 101.4.1"
<1..>321
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="A4D47036.1"
/db_xref="GI:5690321"
/translation="DIVLTQSPATLSVTPGDSVSLSCRASQISNLLHWYQOKSHESP
RLIKYASQISGISIPSRFSGSGSDFTLSINSVETEDFGMYFCQQSNWPLTFGAGT
KLELK"
BASE COUNT 83 a 83 c 73 g 82 t
ORIGIN

Query Match 92.2%; Score 296; DB 94; Length 321;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

CDS
1 GATATTGCTTAACCTACGCTCCAGCCACCTGCTGTGTGACACAGGAGATAGCGTCAGT 60
|||||
1 GATATTGCTTAACCTACGCTCCAGCCACCTGCTGTGTGACCTCCGGAGATAGCGTCAGT 60
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||

Query Match 92.2%; Score 296; DB 94; Length 321;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

CDS
1 GATATTGCTTAACCTACGCTCCAGCCACCTGCTGTGTGACACAGGAGATAGCGTCAGT 60
|||||
1 GATATTGCTTAACCTACGCTCCAGCCACCTGCTGTGTGACTCCAGGAGATAGCGTCAGT 60
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||
```

```

61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
301 GGGACCAAGCTGGAAATTA 320
|||||
301 GGGACCAAGCTGGAGCTTAA 320
|||||

RESULT 4
MUSCMVH
LOCUS MUSCMVH 321 bp mRNA ROD 26-JUL-1993
DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95945
VERSION M95945.1 GI:309177
KEYWORDS Mus musculus (strain BALB/c, sub_species domesticus) CDNA to mRNA.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 321)
AUTHORS Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S.,
Co, M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L.
TITLE Untitled
JOURNAL Unpublished (1992)
FEATURES
source Location/Qualifiers
1..321
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="MAB 5"
/cell_type="hybridoma"
1..321
mat_peptide
/note="putative"
BASE COUNT 85 a 79 c 77 g 80 t
ORIGIN

Query Match 92.2%; Score 296; DB 94; Length 321;
Best Local Similarity 95.3%; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

CDS
1 GATATTGCTTAACCTACGCTCCAGCCACCTGCTGTGTGACACAGGAGATAGCGTCAGT 60
|||||
1 GATATTGCTTAACCTACGCTCCAGCCACCTGCTGTGTGACTCCGGAGATAGCGTCAGT 60
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCCAAGTCAATCTCGGATCCCTCC 180
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
181 AGGTTCACTGCGAGTGGATCAGGACAGATTCGGTCTCAGTATCAACAGTGTGGAGACT 240
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
241 GAAGATTTTGAAGTATTTCTGTCACAGAGTGGCAGCTGGCCCTCAACAGTTCGGAGGG 300
|||||
301 GGGACCAAGCTGGAGCTTAA 320
|||||
301 GGGACCAAGCTGGAGCTTAA 320
|||||
```

QY 301 GGGACCAAGCTGGAATTA 320  
 |||||  
 Db 301 GGGACCAAGCTGGAATTA 320

RESULT 5  
 MUSIGKXD  
 LOCUS 370 bp mRNA 27-APR-1993  
 DEFINITION Mouse Ig active kappa-chain V-region, partial cds.  
 ACCESSION M93959  
 VERSION M93959.1 GI:197572  
 KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;  
 processed gene.  
 SOURCE Mus musculus cDNA to mRNA.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 370)  
 REFERENCE Takeda, Y., Wise, K.S. and Hoffman, R.W.  
 AUTHORS Nucleotide sequences of immunoglobulin heavy and light chain  
 TITLE V-regions from a monoclonal autoantibody specific for a unique set  
 of small nuclear ribonucleoprotein complexes  
 JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)  
 MEDLINE 92375706  
 FEATURES Location/Qualifiers  
 source  
 1..370  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /map="6"  
 gene 1..370  
 /gene="IgK"  
 CDS 1..370  
 /partial  
 /gene="IgK"  
 /note="putative"  
 /codon\_start=1  
 /function="variable region"  
 /product="immunoglobulin kappa-chain"  
 /protein\_id="AAA39079.1"  
 /db\_xref="GI:554148"  
 /translation="GLMLFWISASRGDIVLTQSPATLSVTPGDVKYSLSCRASQISIN  
 LHWYQKSHESRLLIKVYSQISGIPRFSGSGGTFTLINSVETEDFGWYFCQ  
 SNSWPHFTGSGFKLEIKRADA"  
 BASE COUNT 96 a 90 c 86 g 98 t  
 ORIGIN

Query Match 92.2%; Score 296; DB 94; Length 370;  
 Best Local Similarity 95.3%; Pred. No. 1.5e-90;  
 Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGTCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACGAGATAGCGTCAGT 60  
 |||||  
 Db 37 GATATTGTCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACGAGATAGCGTCAGT 96  
 |||||

QY 61 CTTTCTGCCAGGCCGCAAAAGTATTAGCAACCACTACACTGATGATCAACAAAAATCA 120  
 |||||  
 Db 97 CTTTCTGCCAGGCCGCAAAAGTATTAGCAACCACTACACTGATGATCAACAAAAATCA 156  
 |||||

QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCTCC 180  
 |||||  
 Db 157 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCTCC 216  
 |||||

QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCGCTCTCAGTATCAACAGTGTGGAGACT 240  
 |||||  
 Db 217 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCGCTCTCAGTATCAACAGTGTGGAGACT 276  
 |||||

QY 241 GAAGATTTGGAAATGATTTCTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300  
 |||||  
 Db 277 GAAGATTTGGAAATGATTTCTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 336  
 |||||

QY 301 GGGACCAAGCTGGAATTA 320  
 |||||

Db 337 GGGACCAAGCTGGAATTA 356

RESULT 6  
 E07933  
 LOCUS 381 bp RNA 29-SEP-1997  
 DEFINITION cDNA encoding variable region of mouse anti-FHV-1 antibody L chain.  
 ACCESSION E07933  
 VERSION E07933.1 GI:2176065  
 KEYWORDS JP 1994217786-A/2.  
 SOURCE Mus sp.  
 ORGANISM Mus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 381)  
 REFERENCE Kurumi, K., Maeda, H., Nishiyama, K. and Tokiyoshi, Y.  
 AUTHORS ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT  
 TITLE ENCODING THE SAME ANTIBODY  
 JOURNAL Patent: JP 1994217786-A 2 09-AUG-1994;  
 COMMENT CHEMO SERO THERAPEUT RES INST  
 OS Mus sp. (mouse)  
 PN JP 1994217786-A/2  
 PD 09-AUG-1994  
 PF 28-NOV-1992 JP 1992341255  
 PI KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO, PI  
 TOKIYOSHI YUKIO  
 PC C12P21/08,A61K39/395,C07K15/00,C12N15/13,(C12P21/08,C12R1:91);  
 CC strandedness: Double;  
 CC topology: Linear;  
 CC hypothetical: No;  
 CC anti-sense: No;  
 FH Key  
 FH Location/Qualifiers  
 FT source 1..381  
 /organism="Mus sp."  
 FT mat\_peptide 1..381  
 /product="variable region of mouse anti-FHV-1  
 FT antibody L  
 FT chain'  
 FT Location/Qualifiers  
 source  
 1..381  
 /organism="Mus sp."  
 /db\_xref="taxon:10095"  
 BASE COUNT 94 a 98 c 86 g 103 t  
 ORIGIN

Query Match 92.2%; Score 296; DB 10; Length 381;  
 Best Local Similarity 95.3%; Pred. No. 1.5e-90;  
 Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGTCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACGAGATAGCGTCAGT 60  
 |||||  
 Db 61 GATATTGTCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACGAGATAGCGTCAGT 120  
 |||||

QY 61 CTTTCTGCCAGGCCGCAAAAGTATTAGCAACCACTACACTGATGATCAACAAAAATCA 120  
 |||||  
 Db 121 CTTTCTGCCAGGCCGCAAAAGTATTAGCAACCACTACACTGATGATCAACAAAAATCA 180  
 |||||

QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCTCC 180  
 |||||  
 Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCTCC 240  
 |||||

QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCGCTCTCAGTATCAACAGTGTGGAGACT 240  
 |||||  
 Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCGCTCTCAGTATCAACAGTGTGGAGACT 300  
 |||||

QY 241 GAAGATTTGGAAATGATTTCTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300  
 |||||  
 Db 301 GAAGATTTGGAAATGATTTCTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 360  
 |||||

QY 301 GGGACCAAGCTGGAATTA 320  
 |||||

Db 361 GGGACCAAGCTGGAGCTGAA 380

RESULT 7

LOCUS I131959 381 bp DNA PAT 06-FEB-1997

DEFINITION Sequence 82 from patent US 5585089.

ACCESSION I131959

VERSION I131959.1 GI:1822750

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 381)

AUTHORS Queen, C.L. and Selick, H.E.

TITLE Humanized immunoglobulins

JOURNAL Patent: US 5585089-A 82 17-DEC-1996;

FEATURES Location/Qualifiers

source 1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCCAGGAGATAGCGTCAGT 60

Db 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACCCGGGAGATAGCGTCAGT 120

Qy 61 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

Qy 241 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 300

Db 301 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 360

Qy 301 GGGACCAAGCTGGAAATCAA 320

Db 361 GGGACCAAGCTGGAAATCAA 380

RESULT 8

LOCUS I78571 381 bp DNA PAT 03-APR-1998

DEFINITION Sequence 82 from patent US 5693761.

ACCESSION I78571

VERSION I78571.1 GI:3014725

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 381)

AUTHORS Queen, C.L., Schneider, W.P. and Selick, H.E.

TITLE Polynucleotides encoding improved humanized immunoglobulins

JOURNAL Patent: US 5693761-A 82 02-DEC-1997;

FEATURES Location/Qualifiers

source 1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCCAGGAGATAGCGTCAGT 60

Db 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACCCGGGAGATAGCGTCAGT 120

Qy 61 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

Qy 241 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 300

Db 301 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 360

Qy 301 GGGACCAAGCTGGAAATCAA 320

Db 361 GGGACCAAGCTGGAAATCAA 380

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCCAGGAGATAGCGTCAGT 60

Db 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACTCCGGGAGATAGCGTCAGT 120

Qy 61 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

Qy 241 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 300

Db 301 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 360

RESULT 9

LOCUS I78626 381 bp DNA PAT 03-APR-1998

DEFINITION Sequence 82 from patent US 5693762.

ACCESSION I78626

VERSION I78626.1 GI:3014780

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 381)

AUTHORS Queen, C.L., Co, M. Sung, Schneider, W.P., Landolfi, N.F., Coelingh, K.L.

TITLE Humanized immunoglobulins

JOURNAL Patent: US 5693762-A 82 02-DEC-1997;

FEATURES Location/Qualifiers

source 1..381

BASE COUNT 97 a 92 c 89 g 103 t

ORIGIN

Query Match 92.2%; Score 296; DB 10; Length 381;

Best Local Similarity 95.3%; Pred. No. 1.5e-90;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACACCCAGGAGATAGCGTCAGT 60

Db 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGCTGTGACTCCGGGAGATAGCGTCAGT 120

Qy 61 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120

Db 121 CTTTCCTGCCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 180

Qy 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180

Db 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240

Qy 181 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 AGGTTCACTGGCAGTGGATCAGGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 300

Qy 241 GAAGATTTTGGAAATGTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 300

```

Db 301 GAAGATTGTTGAATGATTCTCTGCTCAACAGAGTAACAGTTGGCTTCACGTTCGGAGGG 360
Qy 301 GGGACCAAGCTGGAAATTA 320 mRNA ROD 26-MAR-1994
Db 361 GGGACCAAGCTGGAAATAA 380

RESULT 10
MUSIGKCNJ 431 bp mRNA ROD 26-MAR-1994
LOCUS Mouse Ig rearranged kappa-chain mRNA, clone AN1LK.
DEFINITION M19913 J03832
ACCESSION M19913.1 GI:197033
VERSION C-region; immunoglobulin light chain; immunoglobulin-kappa;
KEYWORDS processed gene.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 56)
REFERENCE Rule,G.S.
AUTHORS Unpublished (1988)
JOURNAL 2 (bases 1 to 431)
REFERENCE Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
AUTHORS Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
TITLES bodies for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
MEDLINE 86234486
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by
G.Rule, 20-JUL-1988.
FEATURES
source Location/Qualifiers
1. 431
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_type="mature B cell"
33..92
sig_peptide 33..>431
CDS /note="precursor"
/codon_start=1
/product="immunoglobulin kappa-chain"
/protein_id="AAA38888.1"
/db_xref="GI:197034"
/translat="MVPTQILGLMFIWISASRGDIVLTQSPATLSVTPGDVSLSLSCR
ASQSVNHLHWFOQKSHSPRLIKVYASQISGIPRSFGSGCTDTFLINSVETED
FGMYFCQSNWPFPGGKLEIKRADAP"
mat_peptide 93..>431
/product="immunoglobulin kappa-chain"
BASE COUNT 113 a 107 c 102 g 109 t
ORIGIN
Query Match 92.28; Score 296; DB 94; Length 431;
Best Local Similarity 95.38; Pred. No. 1.5e-90;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 1 GATATGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60
Db 93 GATATGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCAGT 152
Qy 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
Db 153 CTTTCCTGCAGGGCCAGCCAAAGTGTAGCAACACCTACACTGGTGTTCACAAAAATCA 212
Qy 121 CATGAGTCTCCAAGCGTTCTCATCAAGTATCGTTCGCCAGTCCACTCTCTGGGATCCCTCC 180
Db 213 CATGAGTCTCCAAGCGTTCTCATCAAGTATCGTTCGCCAGTCCACTCTCTGGGATCCCTCC 272
Qy 181 AGGTTTCAGTGCAGTGCATGACGAGACAGATTTCCGTTCTCAGTATCAACAGTGTGGAGACT 240
Db 273 AGGTTTCAGTGCAGTGCATGACGAGACAGATTTCCGTTCTCAGTATCAACAGTGTGGAGACT 332

```

```

region VK23 (IgG) mRNA, partial cds.
AF139849
VERSION AF139849.1 GI:4732162
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
JOURNAL autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
MEDLINE J. Exp. Med. 190 (5), 691-704 (1999)
PUBMED 99406777
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source
1..324
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/clone="38"
/cell_type="B cell hybridoma (spontaneous fusion with
SP2/0)"
/tissue_type="spleen"
<1..>324
/gene="Igc"
/note="variable region (VJ)"
<1..>324
/gene="Igc"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
VK23"
/protein_id="AAD28636.1"
/db_xref="GI:4732163"
/translation="DIVLTQSPATLSVTPGDVSVLSCRASQISNLSNHWFOQKSHESP
RLIKYASQISIGIPSRFNGSGGDTFTLSINSVETEDFGMYFCQSDNWPHTFGSGT
KLEIKR"
misc_feature 70..105
/note="Igc"
/note="CDR1; complementarity determining region 1"
misc_feature 148..168
/note="Igc"
/note="CDR2; complementarity determining region 2"
misc_feature 265..291
/note="Igc"
/note="CDR3; complementarity determining region 3"
J_segment 287..324
/gene="Igc"
/note="Jk2"
BASE COUNT 87 a 82 c 74 g 81 t
ORIGIN
Query Match 91.7%; Score 294.4; DB 94; Length 324;
Best Local Similarity 95.0%; Pred. No. 5.2e-90;
Matches 304; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1 GATATTGGCTAACTCTCCAGCACCTGCTGTGACACGAGATAGCGTCAGT 60
|||||
DB 1 GATATTGGCTAACTCTCTCCAGCACCTGCTGTGACCTCCAGGATAGCGTCAGT 60
|||||
QY 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGATCAACAAAAATCA 120
|||||
DB 61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGATCAACAAAAATCA 120
|||||
QY 121 CATGAGTCTCCAAGCTTCTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGGATCCCTCC 180
|||||

```

```

Db 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGTTCCCACTCCATCTCTGGGATCCCTCC 180
QY 181 AGGTTCACTGCGAGTGGATCAGGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
|||||
Db 181 AGGTTCAATGCGAGTGGATCAGGGACAGATTTCCTCTCAGTATCAACAGTGTGGAGACT 240
QY 241 GAAGATTTTGAATGATTTCTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
|||||
Db 241 GAAGATTTTGAATGATTTCTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
QY 301 GGGACCAAGCTGGAAATTA 320
|||||
Db 301 GGGACCAAGCTGGAAATTA 320
RESULT 13
LOCUS AF139845 324 bp mRNA ROD 04-NOV-1999
DEFINITION Mus musculus clone 79 immunoglobulin kappa light chain variable
region VK23 (IgG) mRNA, partial cds.
ACCESSION AF139845
VERSION AF139845.1 GI:4732154
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
JOURNAL autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
MEDLINE J. Exp. Med. 190 (5), 691-704 (1999)
PUBMED 99406777
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source
1..324
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/clone="79"
/cell_type="B cell hybridoma (spontaneous fusion with
SP2/0)"
/tissue_type="spleen"
<1..>324
/gene="Igc"
/note="variable region (VJ)"
<1..>324
/gene="Igc"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
VK23"
/protein_id="AAD28632.1"
/db_xref="GI:4732153"
/translation="DIVLTQSPATLSVTPGDVSVLSCRASQISNLSNHWFOQKSHESP
RLIKYASQISIGIPSRFNGSGGDTFTLSINSVETEDFGMYFCQSDNWPHTFGSGT
KLEIKR"
misc_feature 70..105
/note="Igc"
/note="CDR1; complementarity determining region 1"
misc_feature 148..168
/note="Igc"
/note="CDR2; complementarity determining region 2"
misc_feature 265..291
/note="Igc"
/note="CDR3; complementarity determining region 3"
J_segment 287..324
/gene="Igc"

```

```
/codon_start=1
/product="Immunoglobulin kappa light chain variable region
Vk23"
/protein_id="AAD28633.1"
/db_xref="GI:4732157"
/translation="DIVLTQSPATLSVTPGDVSVLSRASQSISSNLHWFQOKSHESP
RLIIKAYQSISGIPSRFNGSGDFTLINSVETEDFGMYFCQSDNWPHTFGSGT
KLEIKR"
misc_feature 70..105
/gene="IgG"
/note="CDR1; complementarity determining region 1"
misc_feature 148..168
/gene="IgG"
/note="CDR2; complementarity determining region 2"
misc_feature 265..291
/gene="IgG"
/note="CDR3; complementarity determining region 3"
J_segment 287..324
/gene="IgG"
/note="JK2"

BASE COUNT 86 a 82 c 75 g 81 t
ORIGIN
-
Query Match 91.2%; Score 292.8; DB 94; Length 324;
Best Local Similarity 94.7%; Pred. No. 1.9e-89;
Matches 303; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GATATTGTCTTAACCTCAGTCTCCAGCCACCCTCTCTGTGACACGAGATAGCGTCAGT 60
|||||
Db 1 GATATTGTCTTAACCTCAGTCTCCAGCCACCCTCTCTGTGACCTCCAGGAGATAGCGTCAGT 60
|||||

QY 61 CTTTCTCGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
Db 61 CTTTCTCGCCAGGCCAGCCAAAGTATTAGCAGCAACCTACACTGGTTTCAACAGAAATCA 120
|||||

QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
|||||
Db 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
|||||

QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
|||||
Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
|||||

QY 241 GAAGATTTTGGAAATGATTTCTCTCAACAGAGTGGCCTCCACACGTTTCGGAGGG 300
|||||
Db 241 GAAGATTTTGGAAATGATTTCTCTCAACAGAGTGGCCTCCACACGTTTCGGAGGG 300
|||||

QY 301 GGGACCAAGCTGGAATTTAA 320
|||||
Db 301 GGGACCAAGCTGGAATTTAA 320
|||||

RESULT 15
MMU277215 321 bp mRNA ROD 24-NOV-2000
LOCUS Mus musculus partial mRNA for immunoglobulin light chain variable
DEFINITION region, clone 1G11.
ACCESSION AJ277215
VERSION AJ277215.1 GI:7529622
KEYWORDS immunoglobulin light chain; monoclonal antibody; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Gilbert,D., Lopez,B., Parain,J., Koutourov,S. and Tron,F.
TITLE Overlap of the anti-cardiolipin and anti-nucleosome responses of
the (NZW x BXSB)F1 mouse strain: a new pattern of cross-reactivity
for lupus-related autoantibodies
JOURNAL Eur. J. Immunol. 30 (11), 3271-3280 (2000)
MEDLINE 20545209
REFERENCE 2 (bases 1 to 321)

BASE COUNT 86 a 82 c 75 g 81 t
ORIGIN
-
Query Match 91.2%; Score 292.8; DB 94; Length 324;
Best Local Similarity 94.7%; Pred. No. 1.9e-89;
Matches 303; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GATATTGTCTTAACCTCAGTCTCCAGCCACCCTCTCTGTGACACGAGATAGCGTCAGT 60
|||||
Db 1 GATATTGTCTTAACCTCAGTCTCCAGCCACCCTCTCTGTGACCTCCAGGAGATAGCGTCAGT 60
|||||

QY 61 CTTTCTCGCCAGGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120
|||||
Db 61 CTTTCTCGCCAGGCCAGCCAAAGTATTAGCAGCAACCTACACTGGTTTCAACAGAAATCA 120
|||||

QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
|||||
Db 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCAGTCCATCTCTGGGATCCCTCC 180
|||||

QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
|||||
Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACT 240
|||||

QY 241 GAAGATTTTGGAAATGATTTCTCTCAACAGAGTGGCCTCCACACGTTTCGGAGGG 300
|||||
Db 241 GAAGATTTTGGAAATGATTTCTCTCAACAGAGTGGCCTCCACACGTTTCGGAGGG 300
|||||

QY 301 GGGACCAAGCTGGAATTTAA 320
|||||
Db 301 GGGACCAAGCTGGAATTTAA 320
|||||

RESULT 14
AF139846 324 bp mRNA ROD 04-NOV-1999
LOCUS Mus musculus clone 15 immunoglobulin kappa light chain variable
DEFINITION region Vk23 (IgG) mRNA, partial cds.
ACCESSION AF139846
VERSION AF139846.1 GI:4732156
KEYWORDS house mouse.
SOURCE Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
Location/Qualifiers
1..324
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/chromosome="6"
/clone="15"
/cell_type="B cell hybridoma (spontaneous fusion with
SP2/O)"
/tissue_type="spleen"
<1..>324
/gene="IgG"
/note="variable region (VJ)"
<1..>324
/gene="IgG"
```

Search completed: October 11, 2001, 15:09:32  
Job time: 6354 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 14:34:04 ; Search time 2341.88 seconds  
(without alignments)  
1295.697 Million cell updates/sec

Title: US-08-791-391A-7  
Perfect score: 321  
Sequence: 1 GATATTGCTGAACCTAGTC.....GGACCAAGCTGGAATTAAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est33:\*  
26: gb\_est34:\*  
27: gb\_est35:\*  
28: gb\_est36:\*  
29: gb\_est37:\*  
30: gb\_est38:\*  
31: gb\_est39:\*  
32: gb\_est40:\*  
33: em\_estba:\*  
34: em\_estfun:\*  
35: em\_esthum1:\*  
36: em\_esthum2:\*  
37: em\_esthum3:\*  
38: em\_esthum4:\*  
39: em\_esthum5:\*  
40: em\_esthum6:\*  
41: em\_esthum7:\*  
42: em\_esthum8:\*  
43: em\_esthum9:\*

em\_esthum10:\*  
44: em\_esthum11:\*  
45: em\_esthum12:\*  
46: em\_esthum13:\*  
47: em\_esthum14:\*  
48: em\_esthum15:\*  
49: em\_esthum16:\*  
50: em\_esthum17:\*  
51: em\_esthum18:\*  
52: em\_esthum19:\*  
53: em\_esthum20:\*  
54: em\_esthum21:\*  
55: em\_esthum22:\*  
56: em\_esthum23:\*  
57: em\_esthum24:\*  
58: em\_esthum25:\*  
59: em\_esthum26:\*  
60: em\_esthum27:\*  
61: em\_esthum28:\*  
62: em\_estin1:\*  
63: em\_estin2:\*  
64: em\_estin3:\*  
65: em\_estin4:\*  
66: em\_estin5:\*  
67: em\_estom1:\*  
68: em\_estom2:\*  
69: em\_estov1:\*  
70: em\_estov2:\*  
71: em\_estpl1:\*  
72: em\_estpl2:\*  
73: em\_estpl3:\*  
74: em\_estpl4:\*  
75: em\_estpl5:\*  
76: em\_estpl6:\*  
77: em\_estpl7:\*  
78: em\_estpl8:\*  
79: em\_estpl9:\*  
80: em\_estpl10:\*  
81: em\_estro1:\*  
82: em\_estro2:\*  
83: em\_estro3:\*  
84: em\_estro4:\*  
85: em\_estro5:\*  
86: em\_estro6:\*  
87: em\_estro7:\*  
88: em\_estro8:\*  
89: em\_estro9:\*  
90: em\_estro10:\*  
91: em\_estro11:\*  
92: em\_estro12:\*  
93: em\_estro13:\*  
94: em\_estro14:\*  
95: em\_estro15:\*  
96: em\_estro16:\*  
97: em\_estro17:\*  
98: em\_estro18:\*  
99: em\_estro19:\*  
100: em\_estro20:\*  
101: gb\_est25:\*  
102: gb\_est26:\*  
103: gb\_est27:\*  
104: gb\_est28:\*  
105: gb\_est29:\*  
106: gb\_est30:\*  
107: gb\_est31:\*  
108: gb\_est32:\*  
109: gb\_est41:\*  
110: gb\_est42:\*  
111: gb\_est43:\*  
112: gb\_est44:\*  
113: gb\_est45:\*  
114: gb\_est46:\*  
115: gb\_est47:\*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est67:\*  
137: gb\_est68:\*  
138: gb\_est69:\*  
139: gb\_est70:\*  
140: gb\_est71:\*  
141: gb\_est72:\*  
142: gb\_est73:\*  
143: gb\_est74:\*  
144: gb\_est75:\*  
145: gb\_est76:\*  
146: gb\_est77:\*  
147: gb\_est78:\*  
148: gb\_est79:\*  
149: gb\_est80:\*  
150: gb\_est81:\*  
151: gb\_est82:\*  
152: gb\_est83:\*  
153: gb\_est84:\*  
154: gb\_est85:\*  
155: gb\_est86:\*  
156: gb\_est87:\*  
157: gb\_est88:\*  
158: gb\_est89:\*  
159: gb\_est90:\*  
160: gb\_est91:\*  
161: gb\_est92:\*  
162: gb\_est93:\*  
163: gb\_est94:\*  
164: gb\_est95:\*  
165: gb\_est96:\*  
166: gb\_est97:\*  
167: gb\_est98:\*  
168: gb\_est99:\*  
169: gb\_est100:\*  
170: gb\_est101:\*  
171: gb\_est102:\*  
172: gb\_est103:\*  
173: gb\_est104:\*  
174: gb\_est105:\*  
175: gb\_est106:\*  
176: gb\_est107:\*  
177: gb\_est108:\*  
178: gb\_est109:\*  
179: gb\_est110:\*  
180: gb\_est111:\*  
181: gb\_est112:\*  
182: gb\_est113:\*  
183: gb\_est114:\*  
184: gb\_est115:\*  
185: gb\_est116:\*  
186: gb\_est117:\*  
187: gb\_est118:\*  
188: gb\_est119:\*  
189: gb\_est120:\*

190: gb\_est121:\*  
191: gb\_est122:\*  
192: gb\_est123:\*  
193: gb\_est124:\*  
194: gb\_est125:\*  
195: gb\_est126:\*  
196: gb\_est127:\*  
197: gb\_est128:\*  
198: gb\_est129:\*  
199: gb\_est130:\*  
200: gb\_est131:\*  
201: gb\_est132:\*  
202: gb\_est133:\*  
203: gb\_est134:\*  
204: gb\_est135:\*  
205: gb\_est136:\*  
206: gb\_est137:\*  
207: gb\_est138:\*  
208: gb\_est139:\*  
209: gb\_est140:\*  
210: gb\_est141:\*  
211: gb\_est142:\*  
212: gb\_est143:\*  
213: gb\_est144:\*  
214: gb\_est145:\*  
215: gb\_est146:\*  
216: gb\_est147:\*  
217: gb\_est148:\*  
218: gb\_est149:\*  
219: gb\_est150:\*  
220: gb\_est151:\*  
221: gb\_est152:\*  
222: gb\_est153:\*  
223: gb\_est154:\*  
224: gb\_est155:\*  
225: gb\_est156:\*  
226: gb\_est157:\*  
227: gb\_est158:\*  
228: gb\_est159:\*  
229: gb\_est160:\*  
230: gb\_est161:\*  
231: gb\_est162:\*  
232: gb\_est163:\*  
233: gb\_est164:\*  
234: gb\_est165:\*  
235: gb\_est166:\*  
236: gb\_est167:\*  
237: gb\_est168:\*  
238: gb\_est169:\*  
239: gb\_est170:\*  
240: gb\_est171:\*  
241: gb\_est172:\*  
242: gb\_est173:\*  
243: gb\_est174:\*  
244: gb\_est175:\*  
245: gb\_est176:\*  
246: gb\_est177:\*  
247: gb\_est178:\*  
248: gb\_est179:\*  
249: gb\_est180:\*  
250: gb\_est181:\*  
251: gb\_est182:\*  
252: gb\_est183:\*  
253: gb\_est184:\*  
254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	266	82.9	738	150	BF582153 602099743
2	255.6	79.6	949	150	BF579007 602096124
3	233.6	72.8	624	166	BE306691 601104076
4	223.8	69.7	849	150	BF583521 602101553
5	204	63.6	708	166	BE309445 601095331
6	194.4	60.6	434	115	AW406486 UI-HF-BLO
7	192	59.8	946	155	EG569760 602590367
8	190.4	59.3	519	115	AW405183 UI-HF-BLO
9	188.8	58.8	398	115	AW405309 UI-HF-BLO
10	187.2	58.3	465	115	AW404697 UI-HF-BLO
11	187.2	58.3	468	115	AW404506 UI-HF-BLO
12	185.8	57.9	385	115	AW405025 UI-HF-BLO
13	185.6	57.8	468	115	AW405643 UI-HF-BLO
14	185.6	57.8	482	32	AV733856
15	185.6	57.8	1015	155	EG536848 602566386
16	184.6	57.5	936	145	BF164906 601778137
17	184	57.3	514	115	AW405207 UI-HF-BLO
18	181.4	56.5	548	155	EG568486 602587455
19	180.8	56.3	615	122	AW959456 EST371526
20	180.6	56.3	1061	151	BF663663 602145371
21	179.6	56.0	330	115	AW406212 UI-HF-BLO
22	179.2	55.8	448	115	AW404726 UI-HF-BLO
23	179.2	55.8	485	110	AV734882
24	179	55.8	451	170	BF874574 IL3-ET011
25	178.4	55.6	639	32	AV734416
26	177.6	55.3	409	115	AW406057 UI-HF-BLO
27	177.6	55.3	461	115	AW406219 UI-HF-BLO
28	176.6	55.0	868	155	EG539952 602567464
29	175.4	54.6	413	115	AW406440 UI-HF-BLO
30	175.4	54.6	489	115	AW406154 UI-HF-BLO
31	175.4	54.6	656	154	EG482934 602502942
32	174.6	54.4	576	115	AW378342 RCO-HT021
33	174.4	54.3	443	115	AW405460 UI-HF-BLO
34	174.4	54.3	748	154	EG529887 602558987
35	174.2	54.3	758	154	EG534598 602553450
36	173	53.9	317	115	AW404261 UI-HF-BLO
37	172.6	53.8	504	115	AW405787 UI-HF-BLO
38	171	53.3	369	115	AW405943 UI-HF-BLO
39	170	53.0	473	115	AW406934 UI-HF-BLO
40	169.6	52.8	425	115	AW406785 UI-HF-BLO
41	169.6	52.8	514	169	BF747264 RCL-BT025
42	169.6	52.8	604	115	AW405198 UI-HF-BLO
43	169.4	52.8	518	115	AW406576 UI-HF-BLO
44	169.4	52.8	644	115	AW405817 UI-HF-BLO
45	169.4	52.8	661	32	AV693657

ALIGNMENTS

Result No.	Score	Query Match %	Length	DB ID	Description
1	266	82.9	738	150	BF582153 602099743
2	255.6	79.6	949	150	BF579007 602096124
3	233.6	72.8	624	166	BE306691 601104076
4	223.8	69.7	849	150	BF583521 602101553
5	204	63.6	708	166	BE309445 601095331
6	194.4	60.6	434	115	AW406486 UI-HF-BLO
7	192	59.8	946	155	EG569760 602590367
8	190.4	59.3	519	115	AW405183 UI-HF-BLO
9	188.8	58.8	398	115	AW405309 UI-HF-BLO
10	187.2	58.3	465	115	AW404697 UI-HF-BLO
11	187.2	58.3	468	115	AW404506 UI-HF-BLO
12	185.8	57.9	385	115	AW405025 UI-HF-BLO
13	185.6	57.8	468	115	AW405643 UI-HF-BLO
14	185.6	57.8	482	32	AV733856
15	185.6	57.8	1015	155	EG536848 602566386
16	184.6	57.5	936	145	BF164906 601778137
17	184	57.3	514	115	AW405207 UI-HF-BLO
18	181.4	56.5	548	155	EG568486 602587455
19	180.8	56.3	615	122	AW959456 EST371526
20	180.6	56.3	1061	151	BF663663 602145371
21	179.6	56.0	330	115	AW406212 UI-HF-BLO
22	179.2	55.8	448	115	AW404726 UI-HF-BLO
23	179.2	55.8	485	110	AV734882
24	179	55.8	451	170	BF874574 IL3-ET011
25	178.4	55.6	639	32	AV734416
26	177.6	55.3	409	115	AW406057 UI-HF-BLO
27	177.6	55.3	461	115	AW406219 UI-HF-BLO
28	176.6	55.0	868	155	EG539952 602567464
29	175.4	54.6	413	115	AW406440 UI-HF-BLO
30	175.4	54.6	489	115	AW406154 UI-HF-BLO
31	175.4	54.6	656	154	EG482934 602502942
32	174.6	54.4	576	115	AW378342 RCO-HT021
33	174.4	54.3	443	115	AW405460 UI-HF-BLO
34	174.4	54.3	748	154	EG529887 602558987
35	174.2	54.3	758	154	EG534598 602553450
36	173	53.9	317	115	AW404261 UI-HF-BLO
37	172.6	53.8	504	115	AW405787 UI-HF-BLO
38	171	53.3	369	115	AW405943 UI-HF-BLO
39	170	53.0	473	115	AW406934 UI-HF-BLO
40	169.6	52.8	425	115	AW406785 UI-HF-BLO
41	169.6	52.8	514	169	BF747264 RCL-BT025
42	169.6	52.8	604	115	AW405198 UI-HF-BLO
43	169.4	52.8	518	115	AW406576 UI-HF-BLO
44	169.4	52.8	644	115	AW405817 UI-HF-BLO
45	169.4	52.8	661	32	AV693657

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM9801 row: f column: 11  
High quality sequence source: 714.  
Location/Qualifiers  
1. .738  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4219402"  
/lab\_host="DHI10B (T1 phage-resistant)"  
/site="organ: colon; Vector: pcMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 210 a 189 c 172 g 167 t  
ORIGIN  
Query Match 82.9%; Score 266; DB 150; Length 738;  
Best Local Similarity 94.0%; Pred No. 2e-74; Indels 4; Gaps 2;  
Matches 299; Conservative 0; Mismatches 15;  
QY 6 TGTGTAAGTCTCCAGCCACCTGTCGTGTGACACGAGATAGCGTCAGTCTTTC 65  
Db 78 TGTGTAAGTCTCCAGCCACCTGTCGTGTGACACGAGATAGCGTCAGTCTTTC 137  
QY 66 CTGCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAATCATGA 125  
Db 138 CTGCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAATCATGA 197  
QY 126 GTCCTCAAGCTTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCCAGGTT 185  
Db 198 GTCCTCAAGCTTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCCAGGTT 257  
QY 186 CAGTGGCAGTGGATCAGGACAGATTTTCGTCTCAGTATCAACAGTGTGGAGACTGAAGA 245  
Db 258 CAGTGGCAGTGGATCAGGACAGATTTTCGTCTCAGTATCAACAGTGTGGAGACTGAAGA 317  
QY 246 TTTTGGATGATTTCTGTCAACAGAGTGGAGTGGGCTCA---CACGTTGGAGGGGG 302  
Db 318 -TTTGGATGATTTCTGTCAACAGAGTAAACAGTGGGCTCAGCTCAGCTTCGGTCTGG 376  
QY 303 GACCAAGCTGGAAATTA 320  
Db 377 GACCAAGCTGGAGCTGA 394  
RESULT 2  
BF579007 949 bp mRNA EST 12-DEC-2000  
LOCUS 602096124F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4216180 5',  
DEFINITION mRNA sequence.  
ACCESSION BF579007  
VERSION BF579007.1 GI:11652719  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 949)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LHAM9792 row: p column: 05  
High quality sequence start: 9  
High quality sequence stop: 730.

FEATURES  
source Location/Qualifiers

1. .949  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4216180"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DHI0B (TI phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 278 a 241 c 210 g 220 t

Query Match 79.6%; Score 255.6; DB 150; Length 949;  
Best Local Similarity 90.4%; Pred. No. 4.7e-71;  
Matches 284; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
QY 6 TGTGCTAACTCAGTCTCCAGCACCCTGTGTGACACACGAGATAGCGTCAGTCTTTC 65  
Db 83 TGTACTAACTCAGTCTCCAGCACCCTGTGTGACACACGAGATAGCGTCAGTCTTTC 142  
QY 66 CTGCGCAGCGCCAGCAAGTATTAGCAACCACTACACTGCTATCAACAAAAATCACATGA 125  
Db 143 CTGCGAGGCCAGCCAAAGTATTAGCAACCACTACACTGCTATCAACAAAAATCACATGA 202  
QY 126 GTCTCCAAAGGCTTCTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGGATCCCTCCAGGTT 185  
Db 203 GTCTCCAGGCTTCTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGGATCCCTCCAGGTT 262  
QY 186 CAGTGGCAGTGGATCAGGACAGATTCGCTCTCAGTATCAACAGTGTGGAGACTGAAGA 245  
Db 263 CAGTGGCAGTGGATCAGGACAGATTTTCACTCTCAGTATCGCCACTGTGGAGACTGAAGA 322  
QY 246 TTTTGGATGATTTCTGTCAACAGAGTGGCAGCTGCCCTTCACACGTTTCGGAGGGGGAC 305  
Db 323 -TTTGGATGATTTCTGTCTCAGCAGAGTGACAGTTGGCCCGGTCACTGTCGGTCTCTGGGAC 381  
QY 306 CAAGCTGGAATTA 319  
Db 382 CAAACTGGAGCTGA 395

RESULT 3  
BE306691 624 bp mRNA EST 26-OCT-2000  
LOCUS 601104076F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3501355 5',  
DEFINITION mRNA sequence.  
ACCESSION BE306691  
VERSION BE306691.1 GI:9160297  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 624)  
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LHAM8561 row: g column: 20  
High quality sequence stop: 598.

FEATURES  
source Location/Qualifiers

1. .624  
/organism="Mus musculus"  
/strain="CZECH II (feral)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3501355"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary. Stem cell origin."  
/lab\_host="DHI0B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator Providing samples: Gilbert Smith, NIH"  
BASE COUNT 172 a 166 c 145 g 141 t

Query Match 72.8%; Score 233.6; DB 166; Length 624;  
Best Local Similarity 83.1%; Pred. No. 4.8e-64;  
Matches 286; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
QY 1 GATATTGTGTAAGTCTCCAGCACCCTGTGTGACACACGAGATAGCGTCAGT 60  
Db 59 GACATCTGTATGATGACCCAGTCTCCAGCACCCTGTGTGACTCCAGGAGAAACAGTCAGT 118  
QY 61 CTTTCTGCGCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAATCA 120  
Db 119 CTTTCTGTAGGCCAGCCAGAAATATTACAGAAGCTACACTGGTATCAACAGAATCA 178  
QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCACAGTCCATCTCTGGATCCCTCC 180  
Db 179 CATGGACTCCAAAGGCTTCTCATCAAGTATGACACTGATCCCATCTCTGGATCCCTCC 238  
QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTCGCTCTCAGTATCAACAGTGTGGAGACT 240  
Db 239 AGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCTCAGTATCAACAGTGTGAAGCCT 298  
QY 241 GAAGATTTGGATGATTTCTGTCAACAGAGTGGCAGCTGGCCTCACAGTTTCGAGGG 300  
Db 299 GAAGATGAAGGAATATATTACTGTCTTCAAGGTTACAGCATGCCGTATAGTTCCGATCG 358  
QY 301 GGGACCAAGCTGGAATTA 320  
Db 359 GGGACCAAGCTGGAATTA 378

RESULT 4  
BF583521 849 bp mRNA EST 12-DEC-2000  
LOCUS 602101553F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4224853 5',  
DEFINITION mRNA sequence.  
ACCESSION BF583521  
VERSION BF583521  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 849)  
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT

Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM9815 row: 1 column: 14  
 High quality sequence stop: 627.

# FEATURES

source  
 1..849  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4224853"  
 /clone\_lib="NCI\_CGAP\_C024"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 274 a 215 c 183 g 177 t

ORIGIN  
 Query Match 69.7%; Score 223.8; DB 150; Length 849;  
 Best Local Similarity 86.0%; Pred. No. 7.3e-61;  
 Matches 271; Conservative 0; Mismatches 42; Indels 2; Gaps 2;  
 QY 6 TGTGTAAGTCTCCAGCCACCCCTCTGTGTGACACAGGAGATAGCGTCAGCTTTTC 65  
 Db 80 TGTGATGACTAGTCTCCAGCCACCCCTCTGTGTGACTCCAGGATAGTCTCTTTTC 139  
 QY 66 CTGCGAGGCCACCAAGATTATTAGCAACACCTACACTGGTATCAACAAAATCAGTA 125  
 Db 140 CTGCGAGGCCACCAAGATTATTAGCAACATTTACACTGGTATCAACAAATATCATGA 199  
 QY 126 GTCCTCAAGGCTTTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCCAGGTT 185  
 Db 200 GTCCTCAAGGCTTTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCCAGGTT 259  
 QY 186 CAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGGAGACTGAAGA 245  
 Db 260 CAGTGGCAGTGGATCAGGTCAGATTTTCACTCTCACTATCAACAGTGTGGAACCTGAAGA 319  
 QY 246 TTTTGAATGATTTCTGTCACACAGTGGCAGCTGGCCCTCACAGTTCGGAGGGGGAC 305  
 Db 320 -TGTGGAATTTATTTCTGTCACAAATGGTCACA-ATTTCCGTACACGTTCCGGAGGGGGAC 377  
 QY 306 CAAGCTGGAAATTA 320  
 Db 378 CAAGCTGGAAATTA 392

RESULT 5  
 BE309445 708 bp mRNA EST 26-OCT-2000  
 LOCUS 601095331F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3489991 5',  
 DEFINITION mRNA sequence.  
 BE309445  
 BE309445  
 BE309445.1 GI:9167648  
 EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 708)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM8531 row: n column: 08  
 High quality sequence stop: 575.

# FEATURES

source  
 1..708  
 /organism="Mus musculus"  
 /strain="C57/B6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:3489991"  
 /clone\_lib="NCI\_CGAP\_Mam5"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"  
 BASE COUNT 194 a 180 c 165 g 169 t

ORIGIN  
 Query Match 63.6%; Score 204; DB 166; Length 708;  
 Best Local Similarity 79.4%; Pred. NO. 1.6e-54;  
 Matches 254; Conservative 0; Mismatches 65; Indels 1; Gaps 1;  
 QY 1 GATATTGCTCAACTCAGTCTCCAGCCACCCCTGTGTGACACAGGAGATAGCGTCACT 60  
 Db 65 GACATCTTCTCTCAGTCTCCAGCCACCCCTGTGTGAGTCCAGGAGAAAGTCACT 124  
 QY 61 CTTTCTCTCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAATCA 120  
 Db 125 TTCTCTCGAGGCCCAATCAGATCATTTGSCACAAACATACACTGTATCAGCAAGAACA 184  
 QY 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180  
 Db 185 AATGTTCTTCCAGGCTCCTCATAAAGTATGCTTCTGAGTCTATCTCTGGGATCCCTCC 244  
 QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTCCTCAGTATCAACAGTGTGGAGACT 240  
 Db 245 AGTTTCAGTGGCAGTGGATCAGGACAGATTTTACTCTTAGCATTAACAGTGTAGTCT 304  
 QY 241 GAAGATTTTGAATGATTTCTGTCAACAGAGTGGCAGCTGGCCCTCACAGTTCGGAGGG 300  
 Db 305 GAAGA-TATGCAGATTATTATTGTCAACAAAGTAATAGTGGCCATTACGTTTCGGCTCG 363  
 QY 301 GGGACCAAGCTGGAAATTA 320  
 Db 364 GGGACCAAGCTGGAAATTA 383

RESULT 6  
 AW406486 434 bp mRNA EST 16-FEB-2000  
 LOCUS UI-HF-BL0-act-f-12-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3060238 5', mRNA sequence.  
 AW406486  
 AW406486  
 AW406486.1 GI:6925543  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 434)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL

# THE END



```

VERSION      AW404506.1  GI:6923754
KEYWORDS     EST.
SOURCE       Homo sapiens
ORGANISM     human.
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 465)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              CDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source            1..465
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:305818"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Ronaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      108 a 139 c 115 g 103 t

Query Match      58.3%; Score 187.2; DB 115; Length 465;
Best Local Similarity 74.1%; Pred. No. 3.4e-49;
Matches 237; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY  1  GATATTGCTGAAGTCTCCAGCCACCTGTCTGTGACACAGGAGATAGCGTCAGT 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  85  GAATAGTAGTGGCAGTCTCCAGCCACCTGTCTGTGTCCTCCAGGGGAAAGAGCCACC 144
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  61  CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCTACACCTGGTATCAACAAATCA 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  145  CTCTCTGCCAGGGCCAGTCAGAGTGTAGCAACAACCTAGCCCTGGTACCAAGCAACCT 204
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  121  CATGAGTCTCCAGGCTTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  205  GGCAGGCTCCAGGCTTCATCAATATGTTGGTGCATCCACAGGGCCACTGGTATCCAGCC 264
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  181  AGGTTAGTGGCAGTGGATCAGGACAGATTCGCTCTCAGTATCAACAGTGTGGAGACT 240
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  265  AGGTTAGTGGCAGTGGTCTGGACAGAGTTCACCTCTCACCATCAGCAGCATGCACTCT 324
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  241  GAAGATTTTGGATGATTTCTGTCAACAGAGTGGAGCTGGCTTCACAGTTCGGAGGG 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  325  GAAGATTTTTCAGTTTATTACTGTACAGTATAAATAACTGGCTCTCACTTTTCGGCGGA 384
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  301  GGGACCAAGCTGGAAATTA 320
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  385  GGGACCAAGCTGGAGATCAA 404
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 11
LOCUS     AW404506
DEFINITION UI-HF-BL0-aby-a-05-0-UI.r1 NIH_MGC_37 Homo sapiens CDNA clone
EST      16-FEB-2000

```







Search completed: October 11, 2001, 14:34:05  
Job time: 5542 sec

---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:37 ; Search time 177.65 Seconds  
(without alignments)  
1134.570 Million cell updates/sec

Title: US-08-791-391A-7  
Perfect score: 321  
Sequence: 1 GATATTGCTAACTACGTC.....GGACCAAGCTGGAAATTAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*  
1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT.\*  
3: /SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT.\*  
4: /SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT.\*  
5: /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT.\*  
6: /SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT.\*  
7: /SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT.\*  
8: /SIDS1/gcgdata/geneseq/geneseqn/NA1987.DAT.\*  
9: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT.\*  
10: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT.\*  
11: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT.\*  
12: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT.\*  
13: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT.\*  
14: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT.\*  
15: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT.\*  
16: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT.\*  
17: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT.\*  
18: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT.\*  
19: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT.\*  
20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT.\*  
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT.\*  
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	100.0	321	19 AAV49823	LM609 antibody lig
2	321	100.0	321	22 AAF28178	Antibody LM609 lig
3	296	92.2	381	15 AA064167	Sequence of mouse
4	296	92.2	381	22 AAF58747	Murine CMV5 antio
5	289.6	90.2	5238	11 AA004654	Plasmid pBT111 enc
6	283.2	88.2	381	21 AA235242	Murine vitronectin
7	280	87.2	324	20 AAV71798	Mouse anti-verotox
8	273.6	85.2	324	17 AAT33446	EGF receptor chine
9	268.2	83.6	321	19 AAV49821	Vitaxin antibody l
10	268.2	83.6	321	22 AAF28176	Vitaxin light chai
11	265.8	82.8	321	19 AAV49843	LM609 antibody lig

12	265.6	82.7	651	21 AAA44346	Human secreted exp
13	265.2	82.6	321	22 AAF28199	DNA encoding light
14	259.2	80.7	8858	20 AA210202	Expression vector
15	256	79.8	363	17 AAT38510	Light chain coding
16	254.4	79.3	381	21 AA235244	Humanised anti-ver
17	252.8	78.8	415	21 AAD01262	Mouse monoclonal a
18	241.6	75.3	321	20 AAV71800	Humanised anti-alp
19	241.6	75.3	338	20 AAV71802	Vitronectin alpha-
20	238.4	74.3	415	21 AAD00904	Humanised antibody
21	230.4	71.8	322	15 AA044714	Light chain variab
22	230.4	71.8	322	20 AA228545	Light chain variab
23	224	69.8	321	14 AA043243	B-B10 MAB L chain
24	222.4	69.3	321	19 AAV26766	Anti-gp54 MAB 48-1
25	222.4	69.3	321	21 AAA40203	H. pylori beta-ure
26	222.4	69.3	322	14 AA036615	Anti-IL2R-beta ant
27	222.4	69.3	381	18 AAT49338	CDNA encoding kapp
28	222.4	69.3	415	21 AAD00906	Humanised antibody
29	222.4	69.3	416	18 AAT49344	CDNA encoding kapp
30	222.4	69.3	416	18 AAT49342	CDNA encoding kapp
31	220.8	68.8	486	14 AA043384	L-chain V-region o
32	220.6	68.7	315	20 AAV71803	Jk gene segment.
33	220.6	68.7	315	20 AAV71805	Humanised anti-alp
34	219.4	68.3	318	14 AA048766	Monoclonal antibod
35	219.2	68.3	794	17 AAT42033	Plasmid pMW152-225
36	219.2	68.3	2070	17 AAT42035	Plasmid pSM202-225
37	219.2	68.3	2793	17 AAT42039	Plasmid pMS238-5-2
38	219.2	68.3	2793	17 AAT42040	Plasmid pMS238-225
39	219.2	68.3	3177	17 AAT42041	Plasmid pMS240-5-2
40	218.8	68.2	318	19 AAV54788	DNA encoding the l
41	218.8	68.2	720	19 AAV54790	scfv comprising he
42	217.6	67.8	1395	10 AAN90300	Insert coding for
43	216.6	67.5	720	19 AAV26770	Anti-gp54 MAB 48-1
44	216	67.3	381	19 AAV12262	Monoclonal antibod
45	214.4	66.8	717	14 AA040463	Fv(TU25). Homo sa

## ALIGNMENTS

RESULT 1  
AAV49823  
ID AAV49823 standard; DNA; 321 BP.  
XX AC AAV49823;  
XX AC AAV49823;  
XX DT 02-NOV-1998 (first entry)  
XX DE LM609 antibody light chain variable region DNA fragment.  
XX KW Vitaxin; antibody; variable region; heavy chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; ss.  
XX OS Mus sp.  
XX FH Key Location/Qualifiers  
XX CDS 1..321  
XX FT /\*tag= a  
XX FT /product= "LM609 antibody light chain variable region"  
XX FT /note= "partial sequence, no start or stop codon given"  
XX WO9833919-A2.  
XX PN Sequence of mouse  
XX XX  
XX PD Murine CMV5 antio  
XX XX  
XX PF Plasmid pBT111 enc  
XX XX  
XX PR Murine vitronectin  
XX XX  
XX PR EGF receptor chine  
XX XX  
XX PA Vitaxin antibody l  
XX (IXSY-) IXSYS INC.  
XX LM609 antibody lig



XX Feline herpes virus; FHV-1; monoclonal antibody; CDR;  
KW complementarity determining region; ss.  
XX Mus musculus.

XX Key Location/Qualifiers  
FH CDS 1..381  
FT FT /\*tag= a  
FT misc\_feature 19  
FT /\*tag= b  
FT /label= MKL104  
FT misc\_feature 385..429  
FT /\*tag= c  
FT /label= MJK124

XX W09412661-A.

XX 09-JUN-1994.

XX 25-NOV-1993; 93WO-JP01724.

XX 28-NOV-1992; 92JP-0341255.

XX (KAGA ) CHERO SERO THERAPEUTIC RES INST.

XX Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;

XX WPI; 1994-200288/24.

XX P-PSDB; AAR54093.

XX Feline monoclonal antibody and recombinant antibodies specific  
PT for FHV-1 - for detection, treatment and prevention of FHV-1  
PT infection.

XX Disclosure; Page 18-19; 53pp; Japanese.

XX The inventors claim a monoclonal antibody against feline herpes  
CC virus (FHV-1). They also claim a recombinant antibody against FHV-1  
CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are  
CC used in the detection, treatment and prevention of FHV-1. The  
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1  
CC antibody are given in AAR54093. The sequences of the CDRs in the VL of  
CC the recombinant anti-FHV-1 antibody are given in AAR54093. These CDR  
CC sequences are claimed.

XX Sequence 381 BP; 94 A; 98 C; 86 G; 103 T; 0 other;

Query Match 92.2%; Score 296; DB 15; Length 381;  
Best Local Similarity 95.3%; Pred. No. 4.7e-87;  
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTGAAGTCTGACACCCCTGCTGTGACACCCAGGAGATAGCGTCAGT 60

Db 61 gatattgtctaactcagtcctcagccaccctgtctgtgactcagagatagcgtcagt 120

QY 61 CTTTCTGCGCAGGCGCAGCAAGTATTAGCAACCCACCTACACTGCTATCAACAAATCA 120

Db 121 cttctctgcaggcggccagcaagcattagcaaacaccactggtatcaacaataatca 180

QY 121 CATGAGTCTCAAGGCTTCATCAAGTATTGTTCCAGTCCATCTCTGGGATCCCTCC 180

Db 181 catgagtcctcaagcgttcctcaatcagatgcttcccgactcctctggtatccctcc 240

QY 181 AGGTTAGTGGCAGTGGAGCAGGACAGATTTCTGCTCTCAGTATCAACAGTGTGGAGACT 240

Db 241 aggttcagtggtgagtgagcagggacagatttcactctcagatcaacagtggtgagact 300

QY 241 GAAGATTTTGAAGTATTCTGTGTCACAGAGTGGCAGTGGCTTCACAGTTTCGGAGGG 300

Db 301 gaagattttggaattgtattctgtcaacagagtaaacagctggcctcacacgttcggtgct 360

QY 301 GGGACCAAGCTGGAATTA 320  
Db 361 gggaccaagctggagctgaa 380

RESULT 4

AAF58747  
ID AAF58747 standard; cDNA; 381 BP.

XX AAF58747;

XX 30-APR-2001 (first entry)

DE Murine CMV5 antibody light chain cDNA SEQ ID NO: 82.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;  
KW light chain; graft versus host disease; transplant; autoimmune disease;  
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;  
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection;  
ss.

XX Mus SP.

XX US6180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-0484537.

XX 28-DEC-1988; 88US-0290975.

XX 13-FEB-1989; 89US-0310252.

XX 28-SEP-1990; 90US-0590274.

XX 19-DEC-1990; 90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI; 2001-190856/19.

XX P-PSDB; AAB69687.

XX Producing humanized immunoglobulin, involves producing a cell  
PT containing DNA segments encoding humanized heavy and light chain  
PT variable regions, and expressing the DNA segments in the cell -

XX Example 8; Fig 39; 145pp; English.

XX The present invention describes a method of producing humanised  
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a  
CC humanised version of an immunoglobulin. This is obtained by comparing a  
CC donor and human immunoglobulin and producing a combined antibody which  
CC contains part of each. These are useful in the treatment of  
CC graft-versus-host disease, transplant rejection, autoimmune diseases such  
CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis  
CC and systemic lupus erythematosus, herpes infections, CMV virus infections  
CC and myeloid leukaemia. The present sequence is an antibody cDNA used to  
CC demonstrate the method of the invention.

XX Sequence 381 BP; 97 A; 92 C; 89 G; 103 T; 0 other;

Query Match 92.2%; Score 296; DB 22; Length 381;  
Best Local Similarity 95.3%; Pred. No. 4.7e-87;  
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTGAAGTCTGACACCCCTGCTGTGACACCCAGGAGATAGCGTCAGT 60

Db 61 gatattgtctaactcagtcctcagccaccctgtctgtgactcagggagatagcgtcagt 120

QY 61 CTTTCTGCGCAGGCGCAGCAAGTATTAGCAACCCACCTACACTGCTATCAACAAATCA 120

Db 121 cttctctgcaggcggccagcaagcattagcaaacaccctacactggtatcaacaataatca 180

QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGGATCCCTCC 180  
 Db 181 catgagtcctccaaaggcttctcatcaagtagctctccagtcctctcggatccctcc 240  
 QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGTGGAGACT 240  
 Db 241 agtttcagtggtggtatcaggagacagatttcactctcagtgctcaacggtgtggagact 300  
 QY 241 GAAGATTTTGGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGG 300  
 Db 301 gaagattttgggaatgtattttctgtcaacagagtaaacagtggtggcctcactacgttcggaagg 360  
 QY 301 GGGACCAAGCTGGAATTA 320  
 Db 361 gggaccaagctggaataaa 380

RESULT 5  
 AAQ04654  
 ID AAQ04654 standard; DNA; 5238 BP.  
 AC AAQ04654;  
 XX  
 DT 01-OCT-1990 (first entry)  
 XX  
 DE Plasmid pBT111 encoding antibody MAK33 kappa chain.  
 XX  
 KW Antibody MAK33; kappa chain; plasmid pBT111; activated antibody; ss.  
 XX  
 FH Key Location/Qualifiers  
 CDS 7..663  
 FT /\*tag= a  
 FT /product= kappa chain of MAK33  
 XX  
 PN DE3835350-A.  
 XX  
 PD 19-MAR-1990.  
 XX  
 PF 17-OCT-1988; 88DE-3835350.  
 XX  
 PR 17-OCT-1988; 88DE-3835350.  
 XX  
 PA (BOE ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Rudolph R, Buchner J, Lenz H;  
 XX  
 DR WPI; 1990-156813/21.  
 XX  
 PT Activated antibody prodn. from recombinant procarvotic cells -  
 PT by solubilisation under reducing conditions, then oxidative  
 PT renaturation, carried out at low protein concn.  
 XX  
 PS Disclosure; ; p; German.  
 XX  
 CC Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding  
 CC the fd chain of antibody MAK33 were used to transform E.coli DSM 3689  
 CC and the resulting cells grown to form inclusion bodies. After the final  
 CC renaturation step an 18% yield of biologically-active protein was  
 CC produced.  
 CC see also AAQ04655.  
 XX  
 SQ Sequence 5238 BP; 1276 A; 1359 C; 1411 G; 1192 T; 0 other;

Query Match 90.2%; Score 289.6; DB.11; Length 5238;  
 Best Local Similarity 94.1%; Pred. No. 1.7e-84;  
 Matches 301; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GATATTGCTCAACTGAGTCTCCAGCCACCCCTGTGTGACACAGGAGATAGCTCAGT 60  
 Db 7 gatattgtgctaactcagtcctccagccacccctgtgtgactccaagagatagcgtcagt 66  
 QY 61 CTTTCTCGCCAGGCCCAAGATTATTAGCAACCACTACACTGTGTATCAACAAAAATCA 120

Db 67 ctttctcaggggccagccaaagtatttagcaaacacctacactggtatcaacaaaatca 126  
 QY 121 CATGAGTCTCCAAAGGCTTCTCATCAAGTATCGTTCCTCCAGTCCATCTCTGGGATCCCTCC 180  
 Db 127 catgagtcctccaaaggcttctcatcaaatatgcttccagtcctcctcggatccctct 186  
 QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGTGGAGACT 240  
 Db 187 agtttcagtggtggtatcaggagacagatttcactctcagtcatacaacagtggtggagact 246  
 QY 241 GAAGATTTTGGGAATGTATTTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGG 300  
 Db 247 gaagattttgggaatgtattttctgtcaacagagtaaacagtggtcctcactcagtcgtgct 306  
 QY 301 GGGACCAAGCTGGAATTA 320  
 Db 307 gggaccaagctggagctgaa 326

RESULT 6  
 AAZ35242  
 ID AAZ35242 standard; cDNA; 381 BP.  
 XX  
 AC AAZ35242;  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Mouse anti-verotoxin II antibody VTml-1 VL cDNA.  
 XX  
 KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;  
 KW monoclonal antibody; light chain; mouse; humanised antibody;  
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
 KW HUS; therapy; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 sig\_peptide 1..60  
 FT /\*tag= a  
 FT mat\_peptide 58..381  
 FT /\*tag= b  
 FT /trans\_except= (pos:184..186, aa:Lys)  
 XX  
 PN WO9595629-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 19-MAY-1999; 99WO-US11179.  
 XX  
 PR 20-MAY-1998; 98US-0086570.  
 XX  
 PA (TEIJ ) TEIJIN LTD.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;  
 XX  
 DR WPI; 2000-086580/07.  
 DR P-PSDB; AAZ32405.  
 XX  
 PT Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli -  
 XX  
 PS Disclosure; Fig 1b; 59pp; English.  
 XX  
 CC This DNA sequence codes for the light chain variable region (see  
 CC AA32405) of murine monoclonal antibody VTml-1 (MuVTml-1), an  
 CC antibody that specifically binds to the B subunit of verotoxin II  
 CC (VT2). The invention relates to humanised antibodies against VT2  
 CC that are capable of neutralizing VT2 and/or VT2 variants. The  
 CC humanised antibody is a humanized form of MuVTml-1 comprising the  
 CC complementarity determining regions of MuVTml-1 and heavy and  
 CC light chain variable region frameworks from the human GF4 antibody



CC heavy and light chain frameworks, provided that at least 1 position  
 CC selected from L49, H29, H30, H49 and H98 is occupied by the amino  
 CC acid at the equivalent position of the MuVtm1-1 antibody heavy or  
 CC light chain variable region framework. Such humanized antibodies  
 CC (see AAV32406-07) have an affinity for VT2 that is 3-, 5 or 10-times  
 CC that of MuVtm1-1. They are used for treating a patient suffering  
 CC from, or at risk of, the toxic effects from VT2 (claimed), especially  
 CC for treating verotoxin producing Escherichia coli (VTEC) infection,  
 CC and haemolytic uraemic syndrome (HUS).

XX  
 SQ Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;

Query Match 88.2%; Score 283.2; DB 21; Length 381;  
 Best Local Similarity 92.8%; Pred. No. 7.1e-83;  
 Matches 297; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GATATTGTGCTAACTGCTCCAGCCACCTGCTGTGACACCAGGAGTAGCGTCAGT 60  
 DB 61 gatgtgtgctaaactgctccagccacctgtctgtgactccagagatagcgtcagt 120  
 QY 61 CTTTCTCCGCCAGGCGCAGCAAGTATTAGCAACCCACTACACTGGTATCAACAAAATCA 120  
 DB 121 ctttctcgaggccagctcaactattagcaaacactacactgtatcaacaaatca 180  
 QY 121 CATGAGTCTCCAGGCTTCATCAAGTATGCTGTTCCAGTCCATCTCTGGGATCCCTCC 180  
 DB 181 catgagtctccaggcttcctcatcaagtctgtctccagctccatctctggtatccctcc 240  
 QY 181 AGGTTGAGTGGCAGTGCATGACGAGACAGATTGCTCTCAGTATCAACAGTGGAGACT 240  
 DB 241 aggttcagtgagcagtgatcagggacagatttcaactcagtatcaacagtgtagaact 300  
 QY 241 GAAGATTTTGGAAATGTTCTTCTGTCACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300  
 DB 301 gaagattttggaatgtattctgtcaacagaggttaacagctggccgctcagcttcggtct 360  
 QY 301 GGGACCAAGCTGGAATTA 320  
 DB 361 gggaccaagctggagctgaa 380

AAV71798 standard; cDNA; 324 BP.

AC AAV71798;  
 XT 15-MAR-1999 (first entry)  
 DE Murine vitronectin alpha-v beta-3 receptor MAB VL cDNA.  
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.

XX Mus sp.

OS WO9840488-A1.

PN 17-SEP-1998.

PF 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

XX

DR WPI; 1998-034590/03.  
 DR P-PSDB; AAW84094.

XX New anti alpha.v beta.3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis

XX Example 13; Page 59-60; 97pp; English.

XX This cDNA sequence codes for the light chain variable region (VL,  
 CC see AAW84094) of the anti-human alpha-v beta-3 vitronectin receptor  
 CC murine monoclonal antibody D12. It was obtained from hybridoma  
 CC total RNA by RT-PCR using mouse kappa and N-terminal-based primers  
 CC (see AAV71808-09). A heavy chain variable region clone (see AAV71797)  
 CC has also been identified. D12 VH and VL show sequence similarity  
 CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see  
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see  
 CC AAW84098) were constructed by combining the framework regions of the  
 CC human V region consensus sequences with complementarity determining  
 CC regions of D12 (keeping some preferred murine framework residues).  
 CC The humanised antibodies are specifically reactive with the human  
 CC alpha-v beta-3 protein receptor and capable of neutralising the  
 CC receptor. They can be used for passive immunotherapy of a disorder  
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular  
 CC disorders or angiogenic-related disorders, such as angiogenesis  
 CC associated with diabetic retinopathy, atherosclerosis and  
 CC restenosis, chronic inflammatory disorders, macular degeneration,  
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and  
 CC diseases where bone resorption is associated with pathology such as  
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia  
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone  
 CC loss due to immobilisation or sex hormone deficiency. They can also  
 CC be used for targeted drug therapy, and for detection and diagnosis.

XX Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;

Query Match 87.2%; Score 280; DB 20; Length 324;  
 Best Local Similarity 92.2%; Pred. No. 7.4e-82;  
 Matches 295; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GATATTGTGCTAACTGCTCCAGCCACCTGCTGTGACACCAGGAGTAGCGTCAGT 60  
 DB 1 gatattgtgctaaactgctccagccacctgtctgtgactccagagatagcgtcagt 60  
 QY 61 CTTTCTCCGCCAGGCGCAGCAAGTATTAGCAACCCACTACACTGGTATCAACAAAATCA 120  
 DB 61 ctttctcgaggccagctcaactattagcaaacactacactgtatcaacaaatca 120  
 QY 121 CATGAGTCTCCAGGCTTCATCAAGTATGCTGCCAGTCCATCTCTGGGATCCCTCC 180  
 DB 121 catgagtctccaggcttcctcatcaagtatgtctccagctccatctctggatccctcc 180  
 QY 181 AGGTTGAGTGGCAGTGCATGACGAGACAGATTGCTCTCAGTATCAACAGTGTGGAGACT 240  
 DB 181 aggttcagtgagcagtgatcagggacagatttcaactcagtatcaacatttggagact 240  
 QY 241 GAAGATTTTGGAAATGTTCTTCTGTCACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300  
 DB 241 gaagattttggaatgtattctgtcaacagaggttaacagctggcccttcaacgcttcggtctc 300  
 QY 301 GGGACCAAGCTGGAATTA 320  
 DB 301 gggaccaagctggaaataaa 320

RESULT 8

AAAT33446

ID AAT33446 standard; cDNA; 324 BP.

XX AAT33446;

XX

```

DT 22-NOV-1996 (first entry)
XX EGF receptor chimeric MAb chMint5 VL chain cDNA.
XX
XX Mouse-human chimeric antibody; monoclonal antibody; chMint5;
KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
KW immunotoxin; immunocytokine; tumour; cancer; ss.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1..24
FT /tag= a
FT /note= "primer-derived sequence"
FT misc_feature 301..324
FT /tag= b
FT /note= "primer-derived sequence"
XX
XX WO9627010-A1.
PN
XX
XX 06-SEP-1996.
PD
XX
XX 01-MAR-1996; 96WO-EP00805.
PF
XX
XX 01-MAR-1995; 95IT-OfI0036.
PR
XX
XX (ITU-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
XX
XX Anastasi AM, Colnaghi MT, De Santis R, Di Massimo AM;
PI Ferrer Marsal C, Mele A;
PI
XX WPI: 1996-412776/41.
DR
XX P-PSDB; AAW00241.
XX
XX Murine/human chimeric monoclonal antibody, chMint5 specific for
PT EGF-R - shows a lower immunogenicity when administered to humans
XX
XX Claim 6; Page 17; 28pp; English.
XX
XX A cDNA clone (AA033446) codes for the light chain variable region (VL)
CC (AAW00241) of the epidermal growth factor receptor (EGF-R)-specific
CC mouse-human chimeric antibody chMint5. VH and VL chain sequences
CC were obtd. by PCR amplification of RNA from murine Mint5 hybridoma
CC DSM ACC2150 and fused to human C-gamma and CK genes. Constructs
CC were expressed in CHO cell transfectants. chMint5 shows lower
CC immunogenicity than Mint5 when administered to humans. It can be
CC used in diagnostic assays or used to produce immunotoxins or
CC immunocytokines useful for tumour therapy.
XX
XX Sequence 324 BP; 85 A; 83 C; 78 G; 78 T; 0 other;
SQ

```

---

```

Query Match 85.2%; Score 273.6; DB 17; Length 324;
Best Local Similarity 90.9%; Pred No. 9, 1e-80;
Matches 291; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 GATATTGCTCAACTCAGTCTCCAGCCACCCCTGCTGTGACACCCAGGAGATAGCCTCAGT 60
DB 1 gacatcagctgacccagctccagccaccctgtctgtgactccaggagatagctcagt 60
QY 61 CTTTCTGCGCCAGCCAGCAAGATATTAGCAACCCACTACACTGGTATCAACAAATCA 120
DB 61 cttctctgtagggccagccaaagtattagcaacagcagctcagctggtatcaacaaatca 120
QY 121 CATGAGTCCTCCAGGCTTCTCATCAAGTATGTCCTCCAGTCCATCTCTGGATCCCTCC 180
DB 121 catgagctcccaaggcttctcatcaagtagtattccagctccatctctgtggatccctcc 180
QY 181 AGGTCAGTGGCAGTGGATCAGGAGAGATTTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
DB 181 aggttcagtcgagtcgagtcagggacagatcttcaactctcaactatcaacagtcgtgagact 240
QY 241 GAAGATTTGGGAATGTATTCTTGTCACAGAGTGGCAGCTGCCTCACACGTTCCGAGGG 300

```

---

```

Db 241 aaagatttgggaatgtattctgtcaacagagtgcacagtggtgacagtggtgacgttcgtgga 300
QY 301 GGCACCAACCTGGAAATTAA 320
DB 301 gggaccaagctggatcaaa 320

```

---

```

RESULT 9
AAV49821
ID AAV49821 standard; DNA; 321 BP.
XX
AC AAV49821;
DT 02-NOV-1998 (first entry)
XX
DE Vitaxin antibody light chain variable region DNA.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 1..321
FT /tag= a
FT /product= "vitaxin antibody light chain variable region"
FT /note= "partial sequence, no start or stop codon given"
XX
XX WO9833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX
XX WPI: 1998-437472/37.
DR P-PSDB; AAW76002.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 6; Fig 1b; 129pp; English.
XX
XX This sequence encodes the vitaxin antibody variable light chain region.
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
SQ

```

---

```

Query Match 83.6%; Score 268.2; DB 19; Length 321;
Best Local Similarity 89.7%; Pred No. 5, 2e-78;
Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

```





```

Db 334 gaagatgttgagtgattactgtcaaaatggtcacagcttctccgtacacgttcggagg 393
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
QY 301 GGGACCAAGCTGGAAATTA 320
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
Db 394 gggaccaagctggaaataa 413
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||

RESULT 13
AAF28199
ID AAF28199 standard; DNA; 321 BP.
AC AAF28199;
XX
XX
XX 03-APR-2001 (first entry)
XX
XX DNA encoding light chain variable region of LM609.
XX
XX LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
XX Unidentified.
XX
XX WO200078815-A1.
XX
XX 28-DEC-2000.
XX
XX 23-JUN-2000; 2000WO-US17454.
XX
XX 24-JUN-1999; 99US-0339922.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
XX Huse WD, Wu H;
XX
XX WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
XX Disclosure; Fig 7; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphaVbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 82.68; Score 265.2; DB 22; Length 321;
Best Local Similarity 88.8%; Pred. No. 5e-77;
Matches 285; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 GATATTGTCTTAAGTCTCCAGCCAGCCCTGCTGTGACACCAGGATAGCGTCAGT 60
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
Db 1 gagattgtcctaactcgtctccagccacctgctctcagcaggagaaagggcgact 60
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||

QY 61 CTTTCTCCAGGCCAGCCAGGAAGTATTAGCAACCACTACACTGGTATCAACAAAATCA 120
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
Db 61 ctttcctgccagccagccaaagtattagcaaccactacactggtatcaacaaggcct 120
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||

QY 121 CATGAGTCTCCAGGCTTCTCATAGTATCGTTCCAGTCCATCTCTGGGATCCCTCTC 180
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
```

```

Db 121 ggtcaagcccaaggcttctcatcnnntatcgtttcccaagtcacatctctggatcccgcc 180
QY 181 AGGTTCACTGCGAGTCAGGATCAGGGACACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
Db 181 aggttcagtggtcagtgatcaggacagatttcacccctcactatctccagctctggagcct 240
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
QY 241 GAAGATTTTGGAAATGATTCTGTCAACAGAGTGGCAGCTGCCTTCACACAGTTCGGAGGG 300
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
Db 241 gaagatttgcagtcctattactgtcaacagagtggtcagctggcctccacacgttcggagg 300
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
QY 301 GGGACCAAGCTGGAAATTAAG 321
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||
Db 301 gggaccaagtggaattaag 321
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| |||||

RESULT 14
AAZ10202
ID AAZ10202 standard; DNA; 8858 BP.
XX
XX AAZ10202;
XX
XX 01-NOV-1999 (first entry)
XX
XX Expression vector of light chain of chimeric anti-CD40 antibody chi22.
XX
XX Light chain variable region; chimeric antibody; anti-CD40 antibody;
KW chi220; humoral immune response; T cell dependent antigen;
KW collagen induced arthritis; transplant induced rejection;
KW T cell mediated disorder; autoimmune disease; inflammatory disease;
KW transplantation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT CDS 1085..1388
FT /*tag= a
FT /note= "no termination sequence"
XX
XX WO9942075-A2.
XX
XX 26-AUG-1999.
XX
XX 10-FEB-1999; 99WO-US02949.
XX
XX 19-FEB-1998; 98US-0026291.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;
XX Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;
XX WPI; 1999-527408/44.
XX
XX Antibody that binds human CD40, for treating T cell mediated
PT disorders
XX
XX Claim 18; Fig 14A-C; 77pp; English.
XX
XX The present sequence represents an expression vector for expressing
CC the light chain of a chimeric anti-CD40 antibody designated chi220.
CC The antibodies are effective in modulating humoral immune response
CC against T cell dependent antigens, collagen induced arthritis and
CC transplant induced rejection. They are also useful for their
CC anti-inflammatory properties. The antibodies have wide therapeutic
CC applications, including autoimmune and inflammatory diseases and
CC transplantation. The antibody can be used in a pharmaceutical composition
CC for treating a patient suffering from a T cell mediated disorder. They
CC can also be used to treat autoimmune diseases, inflammatory diseases,
CC and transplantation.
XX
XX Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;
SQ
```

Query Match 80.7%; Score 259.2; DB 20; Length 8858;  
Best Local Similarity 88.1%; Pred. No. 1.8e-74;  
Matches 282; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 GATATTGCTTAACAGTCTCCAGCCAGCCCTGCTGTGACACAGGAGATAGCGTCACT 60  
DB 1065 gacattgttctgactcagctctccagccaccctgtctgtgactccagagatagctct 1124  
QY 61 CTTTCTCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 120  
DB 1125 cttctcagggccagcagagattagcactactacactggtatcaacaaaaatca 1184  
QY 121 CATGAGTCTCCAGGCTTCTCAAGTATGCTTCCCATGCTCATCTGGGATCCCTCC 180  
DB 1185 catgagctccagggcttctcatcaaatatgttccattccatctctggatccctcc 1244  
QY 181 AGGTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGGAGACT 240  
DB 1245 aggttcagtgccagtggtcaggtcagatttcactctcagtcatacaacagtggaacct 1304  
QY 241 GAAGATTTGGGAATGTATTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCCGGAGG 300  
DB 1305 gaagatgttgggaatttattactgtcaaatggtcacagctttccgtggagcttcggtgga 1364  
QY 301 GGGACCAAGCTGGAAATTA 320  
DB 1365 ggcaccaagctggaataca 1384

RESULT 15  
ID AAT38510  
AC AAT38510;  
XX 23-JUN-1997 (first entry)  
XX Light chain coding sequence of monoclonal antibody 4B4-1-1.  
KW Antibody; human; heavy chain; variable region; light chain; MAb; 4-1BB;  
KW tumour necrosis factor receptor; membrane protein; accessory molecule;  
KW T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;  
KW immunosuppressive agent; autoimmune disease; rejection response; therapy;  
KW organ transplantation; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT misc\_feature 1..324  
FT /\*tag= a  
FT /note= "claimed light chain variable region coding  
FT sequence"  
FT misc\_feature 325..363  
FT /\*tag= b  
FT /note= "constant region (encoded protein not given in  
FT specification)"  
XX WO9632495-A1.  
XX 17-OCT-1996.  
XX 06-APR-1996; 96WO-KR00045.  
XX 08-APR-1995; 95KR-0008176.  
XX (GLDS ) LG CHEM LTD.  
XX Kang CY, Kim JG;  
XX WPI; 1996-477145/47.  
XX P-PSDB; AAW04333.  
XX Monoclonal antibody specific for human 4-1BB - useful as

immunospecific agent for treating autoimmune diseases and preventing organ transplant rejection  
Claim 4; Fig 3a; 37pp; English.  
XX AAT38509 and AAT38510 represent the coding sequences for the variable regions of the heavy and light chains of the antibody of the invention. This sequence is stated in the specification as being 372 bp in length, but only comprises 363 bp. The antibody of the invention (designated 4B4-1-1) is a monoclonal antibody (MAb) specific for human 4-1BB. 4-1BB encodes a member of the tumour necrosis factor receptor family of integral membrane proteins. 4-1BB is an accessory molecule expressed on the surface of T-cells in the initial stage of activation. The accessory molecules on the T-cell bind to the corresponding ligand on the antigen-presenting cell and this accelerates the activation of the T- and antigen-presenting cells, thereby promoting various immune responses. The MAb is specific for human 4-1BB, which is selectively expressed on activated T-cells. The MAb is useful as an immunosuppressive agent. It can be used for the treatment of autoimmune diseases, such as rheumatoid arthritis, and for preventing rejection response after organ transplantation.  
XX Sequence 363 BP; 91 A; 102 C; 79 G; 91 T; 0 other;  
SQ Query Match 79.8%; Score 256; DB 17; Length 363;  
Best Local Similarity 87.5%; Pred. No. 5.3e-74;  
Matches 280; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 GATATTGCTTAACAGTCTCCAGCCAGCCCTGCTGTGACACAGGAGATAGCGTCACT 60  
DB 1 gacattgtgtagtaccagctctccagccaccagctgtgactccagagatagctct 60  
QY 61 CTTTCTCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 120  
DB 61 cttctcagggccagcagactattagcacttctacactggtcattcaacaaaaatca 120  
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCCATGCTCTCGGATCCCTCC 180  
DB 121 catgagctccagggcttctcactcaaatatgcttcccaatccatctctggatccctcc 180  
QY 181 AGGTCAGTGGCAGTGGATCAGGACAGATTTGCTCTCAGTATCAACAGTGGAGACT 240  
DB 181 aggttcagtgccagtggtcaggttcagatttcactctcagtcatacaacagtggaacct 240  
QY 241 GAAGATTTGGGAATGTATTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTCCGGAGG 300  
DB 241 gaagatgttggagtggtattactgtcaaatggtcacagctttccctccgagcttcggtgga 300  
QY 301 GGGACCAAGCTGGAAATTA 320  
DB 301 ggcaccaagctggaataca 320

Search completed: October 11, 2001, 15:12:39  
Job time: 6471 sec



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:14:14 ; Search time 87.94 Seconds  
(without alignments)  
891.027 Million cell updates/sec

Title: US-08-791-391A-7

Perfect score: 321

Sequence: 1 GATATTGTGCTAACTAGTC.....GGACCAAGCTGGAAATTAAG 321

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	92.2	381	1	US-07-634-278-82
2	296	92.2	381	1	US-08-477-728-82
3	296	92.2	381	1	US-08-474-040-82
4	296	92.2	381	1	US-08-487-200-82
5	296	92.2	381	4	US-08-484-537-82
6	296	92.2	424	1	US-08-436-463-3
7	289.6	90.2	5238	6	5453363-1
8	256	79.8	324	2	US-08-737-560A-13
9	256	79.8	363	2	US-08-737-560A-8
10	230.4	71.8	322	2	US-08-476-176B-3
11	230.4	71.8	322	3	US-08-127-721A-3
12	230.4	71.8	322	3	US-08-485-246A-3
13	224	69.8	321	2	US-08-232-081B-39
14	219.4	68.3	318	1	US-08-326-362-3
15	218.8	68.2	318	2	US-08-800-198-3
16	218.8	68.2	318	3	US-09-296-595-3
17	218.8	68.2	720	2	US-08-800-198-7
18	218.8	68.2	720	3	US-09-296-595-7
19	216	67.3	720	2	US-07-956-399-1
20	212.2	66.1	429	2	US-08-653-402B-7
21	211.2	65.8	717	2	US-07-956-399-3
22	209.6	65.3	321	1	US-08-192-102-2
23	209.6	65.3	321	1	US-08-324-799-2
24	209.6	65.3	321	2	US-08-132-861A-2
25	196.8	61.3	321	2	US-08-232-081B-35
26	193.6	60.3	321	2	US-08-232-081B-36
27	174.8	54.5	812	1	US-08-053-131-178

ALIGNMENTS

RESULT 1  
US-07-634-278-82  
; Sequence 82, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

Sequence 178, App  
Sequence 41, Appl  
Sequence 19, Appl  
Sequence 201, App  
Sequence 180, App  
Sequence 43, Appl  
Sequence 216, App  
Sequence 107, App  
Sequence 113, App  
Sequence 199, App  
Sequence 211, App  
Sequence 218, App  
Sequence 102, App  
Sequence 105, App  
Sequence 109, App  
Sequence 31, Appl  
Sequence 33, Appl

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-07-634-278-82

Query Match          92.2%; Score 296; DB 1; Length 381;
Best Local Similarity 95.3%; Pred. No. 2e-89;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTCACTCACTCAGTCCAGCCACCCCTGTCTGTGACACCCAGGAGATAGCGTCAGT 60
   |||||||
Db 61 GATATTGCTCACTCACTCAGTCCAGCCACCCCTGTCTGTGACCTCGGAGATAGCGTCAGT 120
   |||||||

QY 61 CTTTCTCGCCAGGCGCAGCAAGTATTAGCAACCCACTACACTGGTATCAACAAAAATCA 120
   |||||||
Db 121 CTTTCTCGAGGCGCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 180
   |||||||

QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCC 180
   |||||||
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCC 240
   |||||||

QY 181 AGTTTCAGTGGCAGTGATCAGGAGAGATTTGGCTCTCAGTATCAACAGTGTGGAGACT 240
   |||||||
Db 241 AGTTTCAGTGGCAGTGATCAGGAGAGATTTTCATCTCAGTGTCAACCGTGTGGAGACT 300
   |||||||

QY 241 GAAGATTTTGGATGTATTCTGTCAACAGAGTGGCCTCAGTGTGGAGGG 300
   |||||||
Db 301 GAAGATTTTGGATGTATTCTGTCAACAGAGTAAAGTGGCCTCATACGTTTCGGAGGG 360
   |||||||

QY 301 GGGACCAAGCTGGAATATA 320
   |||||||
Db 361 GGGACCAAGCTGGAATATA 380
   |||||||

RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-477-728-82

Query Match          92.2%; Score 296; DB 1; Length 381;
Best Local Similarity 95.3%; Pred. No. 2e-89;
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTCACTCACTCAGTCCAGCCACCCCTGTCTGTGACACCCAGGAGATAGCGTCAGT 60
   |||||||
Db 61 GATATTGCTCACTCACTCAGTCCAGCCACCCCTGTCTGTGACCTCGGAGATAGCGTCAGT 120
   |||||||

QY 61 CTTTCTCGCCAGGCGCAGCAAGTATTAGCAACCCACTACACTGGTATCAACAAAAATCA 120
   |||||||
Db 121 CTTTCTCGAGGCGCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 180
   |||||||

QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCC 180
   |||||||
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGATCCCTCC 240
   |||||||

QY 181 AGTTTCAGTGGCAGTGATCAGGAGAGATTTGGCTCTCAGTATCAACAGTGTGGAGACT 240
   |||||||
Db 241 AGTTTCAGTGGCAGTGATCAGGAGAGATTTTCATCTCAGTGTCAACCGTGTGGAGACT 300
   |||||||

QY 241 GAAGATTTTGGATGTATTCTGTCAACAGAGTGGCCTCAGTGTGGAGGG 300
   |||||||
Db 301 GAAGATTTTGGATGTATTCTGTCAACAGAGTAAAGTGGCCTCATACGTTTCGGAGGG 360
   |||||||

QY 301 GGGACCAAGCTGGAATATA 320
   |||||||
Db 361 GGGACCAAGCTGGAATATA 380
   |||||||

RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/474,040  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
US-08-474-040-82

Query Match 92.2% Score 296; DB 1; Length 381;  
Best Local Similarity 95.3%; Pred. No. 2e-89;  
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCCAGGAGATAGCGTCAGT 60  
|||||  
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACCCGGAGATAGCGTCAGT 120  
|||||  
QY 61 CTTTCCTGCCAGGCCAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 120  
|||||  
DB 121 CTTTCCTGCCAGGCCAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 180  
|||||  
QY 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180  
|||||  
DB 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240  
|||||  
QY 241 GAAGATTGGAAATGATTTCTGTCAACAGAGTGGCGCTCAACGTTTCGGAGGG 300  
|||||  
DB 301 GAAGATTGGAAATGATTTCTGTCAACAGAGTAAACAGTTGGCCTCATACGTTCCGAGGG 360  
|||||  
QY 301 GGGACCAAGCTGGAAATTA 320  
|||||  
DB 361 GGGACCAAGCTGGAAATTA 380  
|||||

RESULT 4  
US-08-487-200-82  
; Sequence 82, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLET, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
US-08-487-200-82

Query Match 92.2% Score 296; DB 1; Length 381;  
Best Local Similarity 95.3%; Pred. No. 2e-89;  
Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCCAGGAGATAGCGTCAGT 60  
|||||  
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACCCGGAGATAGCGTCAGT 120  
|||||  
QY 61 CTTTCCTGCCAGGCCAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 120  
|||||  
DB 121 CTTTCCTGCCAGGCCAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAAAATCA 180  
|||||  
QY 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180  
|||||  
DB 181 CATGAGTCTCCAAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240  
|||||  
QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCGCTCTCAGTATCAACAGTGTGGAGACT 240  
|||||

Db 241 AGTTTCAGTGGCAGTGCATCAGGACAGATTTTCACTCTCAGTGTCAACGGTGTGGAGACT 300  
 QY 241 GAAGATTTTGGATGATTTCTCTCAACAGAGTGGCAGCTGCCTCACAGTTTCGAGGG 300  
 Db 301 GAAGATTTTGGATGATTTCTCTCAACAGAGTGGCAGTGTGGCCTCATAGTTTCGAGGG 360  
 QY 301 GGGACCAAGCTGGAATAA 320  
 Db 361 GGGACCAAGCTGGAATAA 380

RESULT 5  
 US-08-484-537-82  
 ; Sequence 82, Application US/08484537  
 ; Patent No. 6180370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: QUEEN, Cary L.  
 ; APPLICANT: CO, Man Sung  
 ; APPLICANT: SCHNEIDER, William P.  
 ; APPLICANT: LANDOLFI, Nicholas F.  
 ; APPLICANT: COELINGH, Kathleen L.  
 ; APPLICANT: SELICK, Harold E.  
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94301

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/484,537  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/634,278  
 ; FILING DATE: 19-DEC-1990  
 ; APPLICATION NUMBER: US 07/590,274  
 ; FILING DATE: 28-SEP-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/310,252  
 ; FILING DATE: 13-FEB-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/290,975  
 ; FILING DATE: 28-DEC-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-002600  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 82:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 381 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..381  
 ; US-08-484-537-82

Query Match 92.2%; Score 296; DB 4; Length 381;  
 Best Local Similarity 95.3%; Pred. No. 2e-89;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 GATATTGCTTAACCTACAGTCTCCAGCCACCCCTCTCTGTGACACCAGGAGATACCGTCAGT 60  
 Db 61 GATATTGCTTAACCTACAGTCTCCAGCCACCCCTCTCTGTGACCCGGAGATACCGTCAGT 120  
 QY 61 CTTTCTCTCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAAATCA 120  
 Db 121 CTTTCTCTCCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTGTATCAACAAAAATCA 180  
 QY 121 CATGAGTCTCCAAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 180  
 Db 181 CATGAGTCTCCAAAGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTCC 240  
 QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240  
 Db 241 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCACTCTCAGTGTCAACGGTGTGGAGACT 300  
 QY 241 GAAGATTTTGGATGATTTCTCTCAACAGAGTGGCAGCTGCCTCACAGTTTCGAGGG 300  
 Db 301 GAAGATTTTGGATGATTTCTCTCAACAGAGTGGCAGTTGGCCTCATAGTTTCGAGGG 360  
 QY 301 GGGACCAAGCTGGAATAA 320  
 Db 361 GGGACCAAGCTGGAATAA 380

RESULT 6  
 US-08-436-463-3  
 ; Sequence 3, Application US/08436463  
 ; Patent No. 5760185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMACHI, Kazuhiko  
 ; APPLICANT: MAEDA, Hiroaki  
 ; APPLICANT: NISHIYAMA, Kiyoto  
 ; APPLICANT: TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: ANTI-EPHILINE HERPES VIRUS-1 RECOMBINANT  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 ; STREET: 419 Seventh Street, N.W., Suite 400  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/436,463  
 ; FILING DATE: 26-JUN-1995  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 341255/1992  
 ; FILING DATE: 28-NOV-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: YON, Allen C.  
 ; REGISTRATION NUMBER: 37,971  
 ; REFERENCE/DOCKET NUMBER: KIMACHI=1  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 424 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:

NAME/KEY: CDS  
LOCATION: 23..403  
US-08-436-463-3

Query Match 92.2%; Score 296; DB 1; Length 424;

Best Local Similarity 95.3%; Pred. No. 2.le-89;

Matches 305; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCCTCCAGCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60  
DB 83 GATATTGCTAACTCAGTCCTCCAGCACCCTGCTGTGACCTCCAGGATAGCGTCAGT 142

QY 61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120  
DB 143 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 202

QY 121 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180  
DB 203 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 262

QY 181 AGGTTCAAGTGCAGTGCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240  
DB 263 AGGTTCAAGTGCAGTGCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 322

QY 241 GAAGATTGGAATGATTCTGTCAACAGAGTGGCAGCTGGCCTCACAGTTCGAGGG 300  
DB 323 GAAGATTGGAATGATTCTGTCAACAGAGTAAACAGTGGCCTCACAGTTCGAGTGT 382

QY 301 GGGACCAAGCTGGAAATTA 320

DB 383 GGGACCAAGCTGGAGCTGAA 402

## RESULT 7

5453363-1

PATENT NO. 5453363

APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; NATTES, RALF

TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR

ING AFTER GENETIC EXPRESSION IN PROKARYOTES

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,044

FILING DATE: 02-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 942,370

FILING DATE: 09-SEP-1992

APPLICATION NUMBER: 498,500

FILING DATE: 23-MAR-1990

APPLICATION NUMBER: 76,207

FILING DATE: 23-OCT-1986

SEQ ID NO: 1:

LENGTH: 5238

5453363-1

Query Match

Best Local Similarity 90.2%; Score 289.6; DB 6; Length 5238;

Matches 301; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCCTCCAGCACCCTGCTGTGACACCAGGAGATAGCGTCAGT 60  
DB 7 gatattgtctaactcagtcctccagccacctgtctgtgactccaagagatagcgtcagt 66

QY 61 CTTTCCTGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAAAATCA 120  
DB 67 ctttcctgagggccagccaaagtattagcaaacacctacactggtatcaacaaaaatca 126

QY 121 CATGAGTCTCAAGGCTTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180  
DB 127 catgagtcctcaagggcttcctcataaataatgcttcctcagtcctcaatctctggatccctct 186

QY 181 AGGTTCAAGTGCAGTGCAGGACAGATTTCCGCTCTCAGTATCAACAGTGTGGAGACT 240

DB 187 aggttcagtgagtgatcagggacagatttcactctcagtatcaacagtgtagagact 246  
QY 241 GAAGATTGGAATGATTCTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300  
DB 247 gaagatttgaatgtattctgtcaacagagtaacagctggcctctcaegttcgggtgct 306  
QY 301 GGGACCAAGCTGGAAATTA 320  
DB 307 gggaccaagctggagctgaa 326

## RESULT 8

US-08-737-560A-13

Sequence 13, Application US/08737560A

Patent No. 5928893

GENERAL INFORMATION:

APPLICANT: KANG, Chang-Yuil

APPLICANT: KIM, Joong-Gon

TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN

TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: KANG, Chang-Yuil

STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,

STREET: Kwanak-gu

CITY: Seoul

STATE: Seoul

COUNTRY: Republic of Korea

ZIP: 151-057

ADDRESSEE: KIM, Joong-Gon

STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu

CITY: Seoul

STATE: Seoul

COUNTRY: Republic of Korea

ZIP: 135-110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage

COMPUTER: IBM PC/AT

OPERATING SYSTEM: MS-DOS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,560A

FILING DATE: 13-NOV-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: KR 95-8176

FILING DATE: 08-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX:

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 324 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

OTHER INFORMATION: polynucleotide encoding 4B4-1-1

OTHER INFORMATION: light chain variable region

US-08-737-560A-13

Query Match

Best Local Similarity 79.8%; Score 256; DB 2; Length 324;

Matches 280; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 GATATTGCTAACTCAGTCTCCAGCCCTGCTGTGTGACACCAGGAGATAGCGTCAGT 60

Db 1 GACATTTGTGATGACCCAGTCTCCAGCCAGTCTGTGACTCCAGGAGATAGAGTCTCT 60  
QY 61 CTTTCTGCGCCAGCCAGCAAGTATTAGCAACCACTACCTGGTATCAACAAAAATCA 120  
Db 61 CTTTCTGCGCCAGCCAGCCAGTATTAGCAACCACTACCTGGTATCAACAAAAATCA 120  
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCTCC 180  
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCTCC 180  
QY 181 AGTTTCAGTGGGAGTGATGAGGACAGATTTGCGTCTCAGTATCAACAGTGTGGAGACT 240  
Db 181 AGTTTCAGTGGGAGTGATGAGGACAGATTTGCGTCTCAGTATCAACAGTGTGGAGACT 240  
QY 241 GAAGATTTTGGAGTGTATTTCTGTCACAGAGTGGCGAGTGGCCTCACACGTTCCGAGGG 300  
Db 241 GAAGATTTTGGAGTGTATTTCTGTCACAGAGTGGCGAGTGGCCTCACACGTTCCGAGGG 300  
QY 301 GGCACCAAGCTGGAATCAA 320  
Db 301 GGCACCAAGCTGGAATCAA 320

RESULT 9

US-08-737-560A-8  
; Sequence 8, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuul  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuul  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; CITY: Kwanak-gu  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 363 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain  
; OTHER INFORMATION: variable region  
; OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1  
; OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2  
; OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3  
; OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region  
US-08-737-560A-8  
  
Query Match 79.8%; Score 256; DB 2; Length 363;  
Best Local Similarity 87.5%; Pred. No. 4.1e-76;  
Matches 280; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
  
QY 1 GATATTGTGCTTAACCTACGTCCTCCAGCCAGTCTGTGTCACACAGGAGATAGAGTCTCT 60  
Db 1 GACATTTGTGATGACCCAGTCTCCAGCCAGTCTGTGACTCCAGGAGATAGAGTCTCT 60  
QY 61 CTTTCTGCGCCAGCCAGCCAGTATTAGCAACCACTACCTGGTATCAACAAAAATCA 120  
Db 61 CTTTCTGCGCCAGCCAGCCAGTATTAGCAACCACTACCTGGTATCAACAAAAATCA 120  
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCTCC 180  
Db 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCCATCTCTGGGATCCCTCC 180  
QY 181 AGTTTCAGTGGGAGTGATGAGGACAGATTTGCGTCTCAGTATCAACAGTGTGGAGACT 240  
Db 181 AGTTTCAGTGGGAGTGATGAGGACAGATTTGCGTCTCAGTATCAACAGTGTGGAGACT 240  
QY 241 GAAGATTTTGGAGTGTATTTCTGTCACAGAGTGGCGAGTGGCCTCACACGTTCCGAGGG 300  
Db 241 GAAGATTTTGGAGTGTATTTCTGTCACAGAGTGGCGAGTGGCCTCACACGTTCCGAGGG 300  
QY 301 GGCACCAAGCTGGAATCAA 320  
Db 301 GGCACCAAGCTGGAATCAA 320

RESULT 10

US-08-476-176B-3  
; Sequence 3, Application US/08476176B  
; Patent No. 5958708  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 5958708man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Immunoglobulin isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5958708artis Patent Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,176B  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/127,721  
; FILING DATE: 27-SEPTEMBER-1993  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..321
; OTHER INFORMATION: /product= "light chain variable
; OTHER INFORMATION: domain of murine antibody TES-C21"
;
; US-08-476-176B-3

Query Match 71.8%; Score 230.4; DB 2; Length 322;
Best Local Similarity 82.5%; Pred. No. 1.3e-67;
Matches 264; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60
DB 1 GACATCTTGTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAGAGTCAGT 60

QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCCTACACTGGTATCAACAAAAATCA 120
DB 61 TTCTCCTGCCAGGCCAGTCCAGCATTTGGCACAACATACACTGGTATCAACAAAGACA 120

QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTTCC 180
DB 121 GATGGTCTCCAGGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCTTCC 180

QY 181 AGGTTTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTTCC 240
DB 181 AGGTTTCTCCAGGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCTTCC 240

QY 241 GAAGATTTTGGATGATTTCTGTCAACAGAGTGGCGAGTGGCTTCAACAGTGTGGAGCT 300
DB 241 GAAGATTTTGGATGATTTCTGTCAACAGAGTGGCGAGTGGCTTCAACAGTGTGGAGCT 300

QY 301 GGGACCAAGCTGGAAATTA 320
DB 301 GGGACCAAGCTGGAGATAAA 320

RESULT 11
US-08-127-721A-3
; Sequence 3, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..321
; OTHER INFORMATION: /product= "light chain variable
; OTHER INFORMATION: domain of murine antibody TES-C21"
;
; US-08-127-721A-3

Query Match 71.8%; Score 230.4; DB 3; Length 322;
Best Local Similarity 82.5%; Pred. No. 1.3e-67;
Matches 264; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACACCAGGAGATAGCGTCAGT 60
DB 1 GACATCTTGTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGAGAAGAGTCAGT 60

QY 61 CTTTCCTGCCAGGCCAGCCAAAGTATTAGCAACACCCTACACTGGTATCAACAAAAATCA 120
DB 61 TTCTCCTGCCAGGCCAGTCCAGCATTTGGCACAACATACACTGGTATCAACAAAGACA 120

QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTTCC 180
DB 121 GATGGTCTCCAGGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCTTCC 180

QY 181 AGGTTTCTCCAGGCTTCTCATCAAGTATCGTTCCAGTCCATCTCTGGGATCCCTTCC 240
DB 181 AGGTTTCTCCAGGCTTCTCATCAAGTATCGTTCTGAGTCTATCTCTGGGATCCCTTCC 240

QY 241 GAAGATTTTGGATGATTTCTGTCAACAGAGTGGCGAGTGGCTTCAACAGTGTGGAGCT 300
DB 241 GAAGATTTTGGATGATTTCTGTCAACAGAGTGGCGAGTGGCTTCAACAGTGTGGAGCT 300

QY 301 GGGACCAAGCTGGAAATTA 320
DB 301 GGGACCAAGCTGGAGATAAA 320

RESULT 12
US-08-485-246A-3
; Sequence 3, Application US/08485246A
; Patent No. 6072035
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6072035man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6072035artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
```





Sequence 3, Application US/08326362  
Patent No. 5730981  
GENERAL INFORMATION:  
APPLICANT: Bosslet, Klaus  
APPLICANT: Seeman, Gerhard  
APPLICANT: Dippold, Wolfgang  
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,  
TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/326,362  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/032,863  
FILING DATE: 17-MAR-1993  
APPLICATION NUMBER: DE P 42 08 795.3  
FILING DATE: 19-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 02481-1276-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-326-362-3

Query Match 68.3%; Score 219.4; DB 1; Length 318;  
Best Local Similarity 80.8%; Pred. No. 5.9e-64;  
Matches 256; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 1 GATATTGCTTAAGTCTCCAGCCAGCCCTGCTGTGACACCCAGGAGATAGGTCAGT 60  
Db 1 GACATCAGCTGACCCAGTCTCCAGCCATCTGCTGTGAGTCCAGGAGAGAGTCAGT 60  
QY 61 CTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCCATACCTGATGTTATCAACAAATCA 120  
Db 61 TTCTCTGCTGGCCAGTCAGAGATTTGGCAGCAGTATACATGTTATCAACAAAGAAC 120  
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180  
Db 121 AATGGTTCTCCAGGCTTCTCATTAAGTATCTCTGAGTCTATCTCTGGATCCCTCC 180  
QY 181 AGGTTAGTGGCAGTGATGAGGAGAGATTTGCTCTCAGTATCAACAGTGGAGACT 240  
Db 181 AGGTTAGTGGCAGTGATGAGGAGAGATTTGCTCTCAGTATCAACAGTGGAGTCT 240  
QY 241 GAGATTTTGAATGATTTCTGTCAACAGAGTGGCAGTGGCTTCACAGTTCGGAGGG 300  
Db 241 GAGATTTTGAATGATTTCTGTCAACAGAGTGGCAGTGGCTTCACAGTTCGGAGGG 300  
QY 301 GGGACCAAGCTGGAAT 317

||||| 11  
Db 301 GGGACCAAGCTGGAGAT 317  
RESULT 15  
US-08-198-3  
Sequence 3, Application US/08800198  
Patent No. 5942602  
GENERAL INFORMATION:  
APPLICANT: WELS, WINFRIED S.  
APPLICANT: SCHMIDT, MATHIAS  
APPLICANT: VAKALOPOULOU, EVANGELIA  
APPLICANT: SCHNEIDER, DOUGLAS  
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,198  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: SCH 1576  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-800-198-3

Query Match 68.2%; Score 218.8; DB 2; Length 318;  
Best Local Similarity 80.5%; Pred. No. 9.4e-64;  
Matches 256; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
QY 1 GATATTGCTTAAGTCTCCAGCCAGCCCTGCTGTGACACCCAGGAGATAGGTCAGT 60  
Db 1 GACATCAGCTGACCCAGTCTCCAGCCATCTGCTGTGAGTCCAGGAGAGAGTCAGT 60  
QY 61 CTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCCATACCTGATGTTATCAACAAATCA 120  
Db 61 TTCTCTGCTGGCCAGTCAGAGATTTGGCAGCAGTATACATGTTATCAACAAAGAAC 120  
QY 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC 180  
Db 121 AATGGTTCTCCAGGCTTCTCATTAAGTATGCTTCTGAGTCTATCTCTGGATCCCTCC 180  
QY 181 AGGTTAGTGGCAGTGATGAGGAGAGATTTGCTCTCAGTATCAACAGTGGAGTCT 240  
Db 181 AGGTTAGTGGCAGTGATGAGGAGAGATTTGCTCTCAGTATCAACAGTGGAGTCT 240  
QY 241 GAGATTTTGAATGATTTCTGTCAACAGAGTGGCAGTGGCTTCACAGTTCGGAGGG 300  
Db 241 GCAGATATTCAGATTTACTGTCAACAAAGTATAGCTGGCCACACGTTTCGGTGTCT 300

QY 301 GGGACCAAGCTGGAATT 318  
||||| ||||| |||||  
Db 301 GGGACCAAGCTGGAATT 318

Search completed: October 11, 2001, 15:14:15  
Job time: 5002 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:09:32 ; Search time 2122.65 Seconds  
(without alignments)  
2339.127 Million cell updates/sec

Title: US-08-791-391A-31  
Perfect score: 321  
Sequence: 1 GAGATTGCTGAACCTCAGTC.....GGACCAAGCTGGAATTAAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl:\*
- 1: gb\_ba1:\*
  - 2: gb\_ba2:\*
  - 3: gb\_ba3:\*
  - 4: gb\_in1:\*
  - 5: gb\_in2:\*
  - 6: gb\_in3:\*
  - 7: gb\_om:\*
  - 8: gb\_ov:\*
  - 9: gb\_pat1:\*
  - 10: gb\_pat2:\*
  - 11: gb\_ph:\*
  - 12: gb\_pl1:\*
  - 13: gb\_pl2:\*
  - 14: gb\_pl3:\*
  - 15: gb\_pl4:\*
  - 16: em\_ba1:\*
  - 17: em\_ba2:\*
  - 18: em\_fun:\*
  - 19: em\_htgo\_hum:\*
  - 20: em\_htgo\_inv:\*
  - 21: em\_htgo\_rod:\*
  - 22: em\_htg\_hum1:\*
  - 23: em\_htg\_hum2:\*
  - 24: em\_htg\_hum3:\*
  - 25: em\_htg\_hum4:\*
  - 26: em\_htg\_hum5:\*
  - 27: em\_htg\_hum6:\*
  - 28: em\_htg\_hum7:\*
  - 29: em\_htg\_hum8:\*
  - 30: em\_htg\_inv1:\*
  - 31: em\_htg\_inv2:\*
  - 32: em\_htg\_other:\*
  - 33: em\_htg\_rod:\*
  - 34: em\_hum1:\*
  - 35: em\_hum2:\*
  - 36: em\_hum3:\*
  - 37: em\_hum4:\*
  - 38: em\_hum5:\*
  - 39: em\_hum6:\*
  - 40: em\_hum7:\*
  - 41: em\_in:\*
  - 42: em\_om:\*
  - 43: em\_or:\*

- 44: em\_ov:\*
- 45: em\_pat:\*
- 46: em\_ph:\*
- 47: em\_pl:\*
- 48: em\_ro:\*
- 49: em\_sts:\*
- 50: em\_sy:\*
- 51: em\_un:\*
- 52: em\_vi:\*
- 53: gb\_sts1:\*
- 54: gb\_sts2:\*
- 55: gb\_sts3:\*
- 56: gb\_sy:\*
- 57: gb\_un:\*
- 58: gb\_vil:\*
- 59: gb\_vil2:\*
- 60: gb\_htg1:\*
- 61: gb\_htg2:\*
- 62: gb\_htg3:\*
- 63: gb\_htg4:\*
- 64: gb\_htg5:\*
- 65: gb\_htg6:\*
- 66: gb\_htg7:\*
- 67: gb\_htg8:\*
- 68: gb\_htg9:\*
- 69: gb\_htg10:\*
- 70: gb\_htg11:\*
- 71: gb\_htg12:\*
- 72: gb\_htg13:\*
- 73: gb\_htg14:\*
- 74: gb\_htg15:\*
- 75: gb\_htg16:\*
- 76: gb\_htg17:\*
- 77: gb\_htg18:\*
- 78: gb\_htg19:\*
- 79: gb\_htg20:\*
- 80: gb\_htg21:\*
- 81: gb\_htg22:\*
- 82: gb\_htg23:\*
- 83: gb\_htg24:\*
- 84: gb\_htg25:\*
- 85: gb\_pr1:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_rol:\*
- 95: gb\_rol2:\*
- 96: gb\_in4:\*
- 97: gb\_pr10:\*
- 98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	318.6	99.3	321	9	AX060782 Sequence
2	318	99.1	321	9	AX060810 Sequence
3	265.8	82.8	321	9	AX060786 Sequence
4	247.2	77.0	321	94	MUSCMVF Mouse mRNA
5	247.2	77.0	321	94	MUSIGKACY M35667 Mouse lysoz
6	247.2	77.0	370	94	MUSIGKXD M93959 Mouse Ig ac
7	245.6	76.5	321	94	AF163757 Mus muscu
8	245.6	76.5	321	94	MUSCMVH M95945 Mouse mRNA

```
9 245.6 76.5 381 10 E07933
10 245.6 76.5 381 10 I31959
11 245.6 76.5 381 10 I78571
12 245.6 76.5 381 10 I78626
13 245.6 76.5 431 94 M05GKCNJ
14 244.4 76.1 324 94 AF139844
15 244 76.0 324 94 AF139849
16 244 76.0 330 94 M05IGL2VK
17 244 76.0 645 94 AB048528
18 242.4 75.5 324 94 AF139845
19 242.4 75.5 324 94 AF139846
20 242.4 75.5 381 94 AF045514
21 242.4 75.5 582 94 M0026998
22 242.4 75.5 738 94 M0040581
23 240.8 75.0 321 94 AF113242
24 240.8 75.0 321 94 AF113243
25 240.8 75.0 321 94 M00277215
26 240.8 75.0 321 94 M00277216
27 240.8 75.0 324 94 AF139847
28 240.8 75.0 324 94 AF139848
29 240.8 75.0 348 94 M0016070
30 240.4 74.9 324 94 M0060469
31 239.6 74.6 420 94 M05IGKCN
32 239.6 74.6 5238 94 A07699
33 239.2 74.5 324 94 AF087031
34 238.6 74.3 317 94 M0016181
35 238 74.1 317 94 M0016181
36 235 73.2 313 94 M05IGVABU
37 234.6 73.1 321 94 M0016181
38 234.4 73.0 381 94 M05IGKAOA
39 234.2 73.0 307 94 AF139235
40 234 72.9 313 94 M05IGVABW
41 233.8 72.8 318 94 M0016181
42 233.6 72.8 323 94 M05ANTDNF
43 233.2 72.6 306 94 M0016181
44 233.2 72.6 315 94 M0086691
45 232.8 72.5 300 94 M05IGRABJ
```

## ALIGNMENTS

```
RESULT 1
AX060782 AX060782 321 bp DNA 22-JAN-2001
LOCUS Sequence 3 from Patent WO0078815. PAT
DEFINITION
ACCESSION AX060782
VERSION AX060782.1 GI:12406162
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1. .321
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..>321
/codon_start=1
/transl_table=11
/protein_id="CAC24889.1"
/db_xref="GI:12406163"
/translation="EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPQOAP
RLIKYRSQISGISGIPARFSGSGSDFTLTITISLEPEDFAVYICQQSGSPHTFGGTT
KVEIK"
```

```
BASE COUNT 78 a 93 c 79 g 71 t
ORIGIN
```

```
Query Match 99.3%; Score 318.6; DB 9; Length 321;
Best Local Similarity 99.1%; Pred. No. 3.4e-86;
Matches 318; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGATTGCTGAAGTCTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
Db 1 GAGATTGCTGAAGTCTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
QY 61 CTTCCTGCGAGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
Db 61 CTTCCTGCGAGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
QY 121 GGTCAAGCCCCAAGGGCTTCATCMKKKTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
Db 121 GGTCAAGCCCCAAGGGCTTCATCAAGTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGTTCGGAGGG 300
Db 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGTTCGGAGGG 300
QY 301 GGGACCAAGGTGGAATAAG 321
Db 301 GGGACCAAGGTGGAATAAG 321

RESULT 2
AX060810 AX060810 321 bp DNA 22-JAN-2001
LOCUS Sequence 31 from Patent WO0078815. PAT
DEFINITION
ACCESSION AX060810
VERSION AX060810.1 GI:12406189
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
JOURNAL encoding same and methods of use
Patent: WO 0078815-A 31 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
source
1. .321
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="grafted antibody variable region"
variation 145..147
BASE COUNT 76 a 93 c 78 g 71 t 3 others
ORIGIN

Query Match 99.1%; Score 318; DB 9; Length 321;
Best Local Similarity 99.1%; Pred. NO. 5.2e-86;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGATTGCTGAAGTCTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
Db 1 GAGATTGCTGAAGTCTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
QY 61 CTTCCTGCGAGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
Db 61 CTTCCTGCGAGCCAGCCAGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
QY 121 GGTCAAGCCCCAAGGGCTTCATCMKKKTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
Db 121 GGTCAAGCCCCAAGGGCTTCATCANNNTATCGTTCACAGTCCATCTCTGGGATCCCCGCC 180
```



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and Brooks, W.B.R.  
TITLE A three-dimensional model of an anti-lysozyme antibody  
JOURNAL J. Mol. Biol. 194, 713-724 (1987)  
MEDLINE 88011212

## FEATURES

Location/Qualifiers  
1..321

/organism="Mus musculus"

/db\_xref="taxon:10090"

<1..>321

/note="lysozyme binding Ig kappa chain V23-J2 region"

/codon\_start=1

/protein\_id="AAA38741.1"

/db\_xref="GI:196585"

/translation="DIVLTQSPATLSVTPGNSVLSRQSGISGNLHWYQKSHESP  
RLIKYASQISGISIPRFSGSGTDTLSINSVETEDFGMYFCQSQSNWPTFFGGT  
KLEIK"

BASE COUNT 88 a 80 c 75 g 78 t

## ORIGIN

Query Match 77.0%; Score 247.2; DB 94; Length 321;  
Best Local Similarity 85.3%; Pred. NO. 1.8e-64;  
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATGTGCTACTAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60

DB 1 GATATTGTGCTACTAGTCTCCAGCCACCCCTGTCTCTCAGGAAATAGCGTCAGT 60

QY 61 CTTCCTGCCAGGCCCAAGATATTAGCAACCACTACCTACCTGGTATCAACAAGGCCT 120

DB 61 CTTCCTGCCAGGCCCAAGATATTAGCAACCACTACCTACCTGGTATCAACAAGGCCT 120

QY 121 GGTCAAGCCCCAAGGCTTCATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGGCC 180

DB 121 CATGAGTCTCAAGGCTTCATCAAGATATGCTTCAGTCCATCTCTGGGATCCCGGCC 180

QY 181 AGGTCAGTGGCAGTGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

DB 181 AGGTCAGTGGCAGTGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

QY 241 GAAGATTTTCAGTCTACTTACTGTCAACAGAGTGGAGTGGCCTCACACGTTCTGGAGGG 300

DB 241 GAAGATTTTCAGTCTACTTACTGTCAACAGAGTGGAGTGGCCTCACACGTTCTGGAGGG 300

QY 301 GGGACCAAGCTGGAATTA 320

DB 301 GGGACCAAGCTGGAATTA 320

RESULT 6

MUSIGKXD MUSIGKXD 370 bp mRNA ROD 27-APR-1993

LOCUS Mouse Ig active kappa-chain V-region, partial cds.

DEFINITION M93959

ACCESSION M93959.1 GI:197572

VERSION V-region; immunoglobulin light chain; immunoglobulin-kappa;

KEYWORDS processed gene.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

TITLE 1 (bases 1 to 370)

REFERENCE Takenai, I., Wise, K.S. and Hoffman, R.W.

JOURNAL Nucleotide sequences of immunoglobulin heavy and light chain

MEDLINE V-regions from a monoclonal autoantibody specific for a unique set

of small nuclear ribonucleoprotein complexes

of Nucleic Acids Res. 20, 4099-4099 (1992)

FEATURES 925/5706 Location/Qualifiers

## source

1..370

/organism="Mus musculus"

/db\_xref="taxon:10090"

/map="6"

1..370

/genes="Igk"

1..370

/partial

/genes="Igk"

/note="putative"

/codon\_start=1

/function="immunoglobulin kappa-chain"

/product="immunoglobulin kappa-chain"

/protein\_id="AAA39079.1"

/db\_xref="GI:554148"

/translation="GLMLFWSASRGDIVLTQSPATLSVTPGDKVLSRQSGISNY

LHWYQKSHESPRLLIKYVSQISIPRFSGSGTDTLSINSVETEDFGMYFCQ

SNSVHTFSGTKLEIKRADA"

BASE COUNT 96 a 90 c 86 g 98 t

## ORIGIN

Query Match 77.0%; Score 247.2; DB 94; Length 370;  
Best Local Similarity 85.3%; Pred. NO. 1.8e-64;  
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTTGCTACTAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60

DB 37 GATATTGTGCTACTAGTCTCCAGCCACCCCTGTCTCTCAGGAGATAAGTCAGT 96

QY 61 CTTCCTGCCAGGCCCAAGATATTAGCAACCACTACCTACCTGGTATCAACAAGGCCT 120

DB 97 CTTCCTGCCAGGCCCAAGATATTAGCAACCACTACCTACCTGGTATCAACAAGGCCT 156

QY 121 GGTCAAGCCCCAAGGCTTCATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGGCC 180

DB 157 CATGAGTCTCAAGGCTTCATCAAGATATGTTTCCAGTCCATCTCTGGGATCCCGGCC 216

QY 181 AGGTCAGTGGCAGTGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

DB 217 AGGTCAGTGGCAGTGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 276

QY 241 GAAGATTTTCAGTCTACTTACTGTCAACAGAGTGGAGTGGCCTCACACGTTCTGGAGGG 300

DB 277 GAAGATTTTCAGTCTACTTACTGTCAACAGAGTAAACAGTGGCCTCATACGTTCTGGAGTCG 336

QY 301 GGGACCAAGCTGGAATTA 320

DB 337 GGGACCAAGCTGGAATTA 356

RESULT 7

AF163757 AF163757 321 bp mRNA ROD 04-AUG-1999

LOCUS Mus musculus mab 101.4.1 immunoglobulin light chain variable region

DEFINITION mRNA, partial cds.

ACCESSION AF163757

VERSION AF163757.1 GI:5690320

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

TITLE 1 (bases 1 to 321)

REFERENCE Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.

JOURNAL Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal

Mertens, N.M. and Cunningham, M.W.

REFERENCE 2 (bases 1 to 321)

AUTHORS Direct Submission

JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma

University Health Sciences Center, 940 St. Young Blvd, Oklahoma

```

FEATURES
  source
    City, OK 73190, USA
    Location/Qualifiers
      1..321
      /organism="Mus musculus"
      /strain="BALB/c"
      /db_xref="taxon:10090"
      /note="Mab 101.4.1"
      <1..>321
      /codon_start=1
      /product="immunoglobulin light chain variable region"
      /protein_id="AAD47036.1"
      /db_xref="GI:5690321"
      /translation="DIVLTQSPATLSVTPGDSVLSRASQISINLNHWQKSHESP
      RLLIKYASQISIGPSRFSGSGDFTLSINSVETEDFGMYFCQSNWPLTFGAGT
      KLELK"
BASE COUNT      83 a   83 c   73 g   82 t
ORIGIN
Query Match      76.5%; Score 245.6; DB 94; Length 321;
Best Local Similarity 85.0%; Pred. NO. 5.5e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

CDS
1 GAGATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCGAGGAGAGGGCGACT 60
|||
1 GATATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCGAGGAGAGGGCGACT 60
|||
61 CTTTCTCTGCCAGGCGAGCAAGTATTAGCAACCACTACACTGCTATCAACAAGGCGCT 120
|||
61 CTTTCTCTGCCAGGCGAGCAAGTATTAGCAACCACTACACTGCTATCAACAAGGCGCT 120
|||
121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCTCAGTCCATCTCTGGGATCCCGCC 180
|||
121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 180
|||
181 AGGTTTCAGTGGCAGTGATCAGGGACAGATTTTCCACCTCAGTCTCAGTCTGGAGCT 240
|||
181 AGGTTTCAGTGGCAGTGATCAGGGACAGATTTTCTCTCAGTCTCAACGGTGTGGAGCT 240
|||
241 GAAGATTTCAGTCTTACTTGTCAACAGAGTGGCAGTGGCCTCAGTCTCGAGGG 300
|||
241 GAAGATTTCAGTCTTACTTGTCTGCAACAGAGTAACTTCTGCTCAGTCTATCGTTCGAGGG 300
|||
301 GGGACCAAGCTGGAAATTA 320
|||
301 GGGACCAAGCTGGAAATTA 320
|||

RESULT 8
MUSCMVH      321 bp mRNA      ROD      26-JUL-1993
LOCUS      Mouse mRNA sequence, partial cds.
ACCESSION      M95945
VERSION      M95945.1 GI:309177
KEYWORDS
SOURCE      Mus musculus (strain BALB/c, sub_species domesticus) CDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 321)
AUTHORS      Simpson,J.A., Chow,J.C., Baker,J., Avdalovic,N.M., Yuan,S.,
Co,M.S., Vasquez,M., Britt,W.J. and Coeligh,K.L.
TITLE      Untitled
JOURNAL      Unpublished (1992)
FEATURES
  source
    Location/Qualifiers
      1..321
      /organism="Mus musculus"
      /strain="BALB/c"
      /sub_species="domesticus"
      /db_xref="taxon:10090"
      /cell_line="Mab 5"
      /cell_type="hybridoma"
      1..321
      mat_peptide

```

```

BASE COUNT      85 a   79 c   77 g   80 t
ORIGIN
Query Match      76.5%; Score 245.6; DB 94; Length 321;
Best Local Similarity 85.0%; Pred. NO. 5.5e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCGAGGAGAGGGCGACT 60
|||
DB 1 GATATTGCTAACTCAGTCTCCAGCCACCTGCTCTGACTCCGGGAGATAGCGTCACT 60
|||
QY 61 CTTTCTCTGCCAGGCGAGCAAGTATTAGCAACCACTACACTGCTATCAACAAGGCGCT 120
|||
DB 61 CTTTCTCTGCCAGGCGAGCAAGTATTAGCAACCACTACACTGCTATCAACAAGGCGCT 120
|||
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCTCAGTCCATCTCTGGGATCCCGCC 180
|||
DB 121 CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 180
|||
QY 181 AGGTTTCAGTGGCAGTGATCAGGGACAGATTTTCCACCTCAGTCTCAGTCTGGAGCT 240
|||
DB 181 AGGTTTCAGTGGCAGTGATCAGGGACAGATTTTCTCTCAGTCTCAACGGTGTGGAGCT 240
|||
QY 241 GAAGATTTCAGTCTTACTTGTCAACAGAGTGGCAGTGGCCTCAGTCTCGAGGG 300
|||
DB 241 GAAGATTTCAGTCTTACTTGTCTGCAACAGAGTAACTTCTGCTCAGTCTATCGTTCGAGGG 300
|||
QY 301 GGGACCAAGCTGGAAATTA 320
|||
DB 301 GGGACCAAGCTGGAAATTA 320
|||

RESULT 9
E07933      381 bp RNA      PAT      29-SEP-1997
LOCUS      cDNA encoding variable region of mouse anti-FHV-1 antibody L chain.
DEFINITION      E07933
ACCESSION      E07933
VERSION      E07933.1 GI:2176065
KEYWORDS      JP 1994217786-A 2 09-AUG-1994;
SOURCE      Mus sp.
ORGANISM      Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 381)
AUTHORS      Kurumi,K., Maeda,H., Nishiyama,K. and Tokiyoshi,Y.
TITLE      ANTI-FELINE HERPES VIRUS-1 RECOMBINANT ANTIBODY AND GENE FRAGMENT
ENCODING THE SAME ANTIBODY
JOURNAL      Patent: JP 1994217786-A 2 09-AUG-1994;
COMMENT      CHEMO SERO THERAPEUT RES INST
OS      Mus sp. (mouse)
PN      JP 1994217786-A/2
PD      09-AUG-1994
PF      28-NOV-1992 JP 1992341255
PI      KURUMI KAZUHIKO, MAEDA HIROAKI, NISHIYAMA KIYOTO, PI
TOKIYOSHI YUKIO
PC      C12P21/08,A61K39/395,C07K15/00,C12N15/13,(C12P21/08,C12R1:91);
CC      strandedness: Double;
CC      topology: Linear;
CC      hypothetical: No;
CC      anti-sense: No;
FH      Key
FH      Location/Qualifiers
FT      source
      1..381
      /organism="Mus sp."
FT      mat_peptide
      1..381
      /product="variable region of mouse anti-FHV-1
      antibody L
      chain".
FT      Location/Qualifiers
      1..381
      /organism="Mus sp."

```

BASE COUNT	94	a	98	c	86	g	103	t	/db_xref="taxon:10095"
ORIGIN									
Query Match	76.5%; Score 245.6; DB 10; Length 381;								
Best Local Similarity	85.0%; Pred. No. 5.4e-64;								
Matches	272;	Conservative	2;	Mismatches	46;	Indels	0;	Gaps	
QY	1	GAGATTGTCTAACTAGTCTCAGCCACCCCTCTGTCTCAGCCAGGAGAAAGGGGAGCT	60						
Db	61	GATATTGTCTAACTAGTCTCCAGCCACCCCTGTCTGTGACTCCAGGAGATAGCGTCAGT	120						
QY	61	CTTTCTCTGCCAGGCGCCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCCT	120						
Db	121	CTTTCTCTGCAGGCGCCAGCAAGTATTAGCAACAACCTACACTGTGTATCAACAATAATCA	180						
QY	121	GGTCAAGCCCCAAGGCTTCTATCMKKTATTCGTTCCAGTCCCATCTCTCTGGGATCCCGCC	180						
Db	181	CATGAGTCTCCAAAGGCTTCATCAAGATATGCTTCCAGTCCCATCTCTGGGATCCCGCTCC	240						
QY	181	AGGTTCAGTGGCAGTGGATCAGGACAGATTTCAACCTCACTATCTCCAGTCTGGAGCCT	240						
Db	241	AGGTTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCAGTATCAACAGTGTGGAGACT	300						
QY	241	GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAACAGTTCGAGGG	300						
Db	301	GAAGATTTTGGATGTATTCTTGTCAACAGAGTAACAGCTGGCCTCACACGTTTCGTTGCT	360						
QY	301	GGGACCAAGGTGGAAATTA	320						
Db	361	GGGACCAAGCTGGAGCTGAA	380						

RESULT	10				PAT
LOCUS	I31959	381 bp	DNA		
DEFINITION	Sequence 82 from patent US 5585089.				
ACCESSION	I31959				
VERSION	I31959.1	GI:1822750			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 381)				
TITLE	Queen,C.I.B. and Selick,H.E.				
JOURNAL	Humanized Immunoglobulins				
FEATURES	Patent: US 5585089-A 82 17-DEC-1996; Location/Qualifiers l..381 /organism="unknown"				
BASE COUNT	97 a   92 c   89 g   103 t				

Query Match	76.5%;	Score 245.6;	DB 10;	Length 381;
Best Local Similarity	85.0%;	Pred. No. 5.4e-64;		
Matches 272;	Conservative 2;	Mismatches 46;	Indels 0;	Gaps
QY 1	GAGATGTTGCTAACTCAGTCTCAGCGCACCCCTGTCTCTCAGCCCGAGGAGAAAGCGGACT	60		
Db 61	GATATTGTGCTAACTCAGTCTCAGCGCACCCCTGTCTGTCTGCTACCTCCGGAGATAGCGTCAGT	120		
QY 61	CTTTCTCGCCAGCGCCAGCAAGTATTAGCACCCAGCTACTGTTATCAACAAAGCGCT	120		
Db 121	CTTTCTCGAGGCCAGCCAAAGTATTAGCACACCTACTGTTATCAACAAATCA	180		
QY 121	GGTCAGCCCCAAGGCTTCTCATCMKKTTATCGTTCGCAGTCCATCTCTGGGATCCCCGCC	180		
Db 181	CATGAGTCTCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCTCC	240		
QY 181	AGGTCAGTGGCAGTGGGATCAGGGACAGATTTCCACCGCTCACTATCTCCAGTCTGGAGCT	240		

Db	241	AGGTTTCAGTGCAGTGGATCAGGACAGATTTCACCTCTCAGCTGTCAACGGTGTGGAGACT	300
Qy	241	GAAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGGCTCTCACAGTTCGGAGGG	300
Db	301	GAAGATTTTGAATGATTTCTGTCAACAGAGTAACAGTTGGCTCTATACGTTTCGGAGGG	360
Qy	301	GGGACCAAGTGGAAATATA	320
Db	361	GGGACCAAGCTGGAAATATA	380

```

RESULT 11
178571
LOCUS 381 bp DNA
DEFINITION Sequence 82 from patent US 5693761.
ACCESSION 178571
VERSION 178571.1 GI:3014725
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 381)
AUTHORS Queen,C.L., Schneider,W.P. and Selick,H.E.
TITLE Polynucleotides encoding improved humanized
JOURNAL immunoglobulins
FEATURES Patent: US 5693761-A 82 02-DEC-1997;
Location/Qualifiers
1.381
source /organism="unknown"
BASE COUNT 97 a 92 c 89 g 103 t
ORIGIN

```

Query Match	76.5%;	Score 245.6;	DB 10;	Length 381;
Best Local Similarity	85.0%;	Pred. No. 5.4e-64;		
Matches 272;	Conservative	2;	Mismatches 46;	Indels 0; Gaps
QY	1	GAGATTGTGCTAACTCAGTCTCAGGCACCCCTGCTCTCAGGCCAGGAGAAAGGGCGACT	60	
DB	61	GATATTGTGCTAACTCAGTCTCAGGCACCCCTGCTCTGACTCCGGGAGTAGCGTCACT	120	
QY	61	CTTTCTGCGCAGGCGACGCGCAAAAGTATTAGCAACCCCTACATGGTGATCAACAAGGCGCT	120	
DB	121	CTTTCTGCGCAGGCGCAGCCAAAGTATTAGCAACAACCTACACTGGTGATCAACAACAAATCA	180	
QY	121	GGTCAAGCCGCCAAGGCTTCATCMKKTATTCGTTCACAGTCCAGTCCATCTCTGGGATCCCGCGC	180	
DB	181	CATGAGTCTCAAGGCTTCATCAAGTATGCTTCCAGTCCCATCTCTGGGATCCCGCTCC	240	
QY	181	AGGTTCACTGCGCAGTGGATCAGGCAGAGATTTTCAACCGCTCACTATCTCCAGTCTGGAGCGCT	240	
DB	241	AGGTTCACTGCGCAGTGGATCAGGCAGAGATTTTCACTCTCAGTGTCAACGGTGTGGAGACT	300	

Qy	301	GGGACCAAGGTGGAAATTA	320			
Db <td>301 <td>GAAGATTTCGAATGATTCTCTCAACAGAGTAACAGTTGGCCTCATACGTTCGGAGG</td> <td>360</td> <td></td> <td></td> <td></td> </td>	301 <td>GAAGATTTCGAATGATTCTCTCAACAGAGTAACAGTTGGCCTCATACGTTCGGAGG</td> <td>360</td> <td></td> <td></td> <td></td>	GAAGATTTCGAATGATTCTCTCAACAGAGTAACAGTTGGCCTCATACGTTCGGAGG	360			
Db <td>361 <td>GGGACCAAGCTGGAAATAA</td> <td>380</td> <td></td> <td></td> <td></td> </td>	361 <td>GGGACCAAGCTGGAAATAA</td> <td>380</td> <td></td> <td></td> <td></td>	GGGACCAAGCTGGAAATAA	380			
RESULT	12					
LOCUS	178626					
DEFINITION	178626	Sequence 82 from patent US 5693762.				
ACCESSION	178626					
VERSION	178626.1	GI:3014780				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 381)					
REVIEWERS	Queen, C. L., Co. M. Seng.					
REVISIONS	Schneider, W. P., Landolfi, N. F., Coelingu					
DATE	03-APR-1998					

REFERENCE  
1 (bases 1 to 381)  
Queen, C. L.; Co. M. Sung, Schneider, W. P.; Landolfi, N. F.; Coelingh, K. L.





```
SP2/0)"
/tissue_type="spleen"
<1..>324
/gene="IgG"
/note="variable region (VJ)"
CDS
<1..>324
/gene="IgG"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
Vk23"
/protein_id="AAD28631.1"
/db_xref="GI:4732153"
/translation="DIVLTQSPATLSVTPGESVLSCRASQSISSLNLHWFQOKSHESP
RLIKYASISGISIPRFSGSGTDFTLSINSVETEDFGMYFQQSDNWPHFGSGT
KLEIKR"
misc_feature 70..105
/gene="IgG"
/note="CDR1; complementarity determining region 1"
misc_feature 148..168
/gene="IgG"
/note="CDR2; complementarity determining region 2"
misc_feature 265..291
/gene="IgG"
/note="CDR3; complementarity determining region 3"
J_segment 287..324
/gene="IgG"
/note="JK2"
BASE COUNT 88 a 82 c 72 g 82 t
ORIGIN
Query Match 76.1%; Score 244.4; DB 94; Length 324;
Best Local Similarity 85.0%; Pred. No. 1.3e-63;
Matches 272; Conservative 1; Mismatches 47; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGCACT 60
|||
Db 1 GATATTGTGCTAACTCAGTCTCAGCCACCCTGTCTGTGACTCCAGGAGAAAGCGTCAGT 60
QY 61 CTTTCTCTGCCAGCGCCAGCAAACTATTAGCAACCACTACACTGGTATCAACAAAGGCCT 120
|||
Db 61 CTTTCTCTGCCAGCGCCAGCAAACTATTAGCAACCACTACACTGGTATCAACAAATCA 120
QY 121 GGTCACAGCCCAAGGCTTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180
|||
Db 121 CATGAGTCTCAAGGCTTCATCAAGTATGCTTCCAGTCCATCTCTGGATCCCGCTCC 180
QY 181 AGTTTCAGTGGCAGTGATCAGGAGAGATTTCACCTCTCACTATCAACAGTGTGGAGCT 240
|||
Db 181 AGTTTCAGTGGCAGTGATCAGGAGAGATTTCACCTCTCACTATCAACAGTGTGGAGCT 240
QY 241 GAAGATTTCAGTCTATTACTCTCAACAGTGGCAGTGGCTCACAGTTCGGAGGG 300
|||
Db 241 GAAGATTTCAGTCTATTACTCTCAACAGTGGCAGTGGCTCACAGTTCGGAGGG 300
QY 301 GGGACCAAGGTGGAATAA 320
|||
Db 301 GGGACCAAGGTGGAATAA 320
RESULT 15
AF139849
LOCUS AF139849 324 bp mRNA ROD 04-NOV-1999
DEFINITION Mus musculus clone 38 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
ACCESSION AF139849
VERSION AF139849.1 GI:4732162
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 324)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source
1..324
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/chromosome="6"
/clone="38"
/cell_type="B cell hybridoma (spontaneous fusion with
SP2/0)"
/tissue_type="spleen"
<1..>324
/gene="IgG"
/note="variable region (VJ)"
<1..>324
/gene="IgG"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
Vk23"
/protein_id="AAD28636.1"
/db_xref="GI:4732163"
/translation="DIVLTQSPATLSVTPGDSVLSCRASQSISSLNLHWFQOKSHESP
RLIKYASQISGISIPRFSGSGTDFTLSINSVETEDFGMYFQQSDNWPHFGSGT
KLEIKR"
misc_feature 70..105
/gene="IgG"
/note="CDR1; complementarity determining region 1"
misc_feature 148..168
/gene="IgG"
/note="CDR2; complementarity determining region 2"
misc_feature 265..291
/gene="IgG"
/note="CDR3; complementarity determining region 3"
J_segment 287..324
/gene="IgG"
/note="JK2"
BASE COUNT 87 a 82 c 74 g 81 t
ORIGIN
Query Match 76.0%; Score 244; DB 94; Length 324;
Best Local Similarity 84.7%; Pred. No. 1.7e-63;
Matches 271; Conservative 2; Mismatches 47; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTCAGTCTCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGCACT 60
|||
Db 1 GATATTGTGCTAACTCAGTCTCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCAGT 60
QY 61 CTTTCTCTGCCAGCGCCAGCAAACTATTAGCAACCACTACACTGGTATCAACAAAGGCCT 120
|||
Db 61 CTTTCTCTGCCAGCGCCAGCAAACTATTAGCAACCACTACACTGGTATCAACAAATCA 120
QY 121 GGTCACAGCCCAAGGCTTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180
|||
Db 121 CATGAGTCTCAAGGCTTCATCAAGTATGCTTCCAGTCCATCTCTGGATCCCGCTCC 180
QY 181 AGTTTCAGTGGCAGTGATCAGGAGAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240
|||
Db 181 AGTTTCAGTGGCAGTGATCAGGAGAGATTTCACCTCTCACTATCTCCAGTCTGGAGCCT 240
QY 241 GAAGATTTCAGTCTATTACTCTCAACAGTGGCAGTGGCTCACAGTTCGGAGGG 300
|||
Db 241 GAAGATTTCAGTCTATTACTCTCAACAGTGGCAGTGGCTCACAGTTCGGAGGG 300
```

Qy 301 GGGACCAAGCTGGAATTAA 320  
|||||||  
Db 301 GGGACCAAGCTGGAATTAA 320

Search completed: October 11, 2001, 15:09:33  
Job time: 6355 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 14:34:05 ; Search time 2341.88 Seconds  
(without alignments)  
1295.697 Million cell updates/sec

Title: US-08-791-391A-31  
Perfect score: 321  
Sequence: 1 GAGATTGCTGAACCTAGTC.....GGACCAAGTGGAATTAAAG 321

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1:	gb_est1:*
2:	gb_est2:*
3:	gb_est3:*
4:	gb_est4:*
5:	gb_est5:*
6:	gb_est6:*
7:	gb_est7:*
8:	gb_est8:*
9:	gb_est9:*
10:	gb_est10:*
11:	gb_est11:*
12:	gb_est12:*
13:	gb_est13:*
14:	gb_est14:*
15:	gb_est15:*
16:	gb_est16:*
17:	gb_est17:*
18:	gb_est18:*
19:	gb_est19:*
20:	gb_est20:*
21:	gb_est21:*
22:	gb_est22:*
23:	gb_est23:*
24:	gb_est24:*
25:	gb_est33:*
26:	gb_est34:*
27:	gb_est35:*
28:	gb_est36:*
29:	gb_est37:*
30:	gb_est38:*
31:	gb_est39:*
32:	gb_est40:*
33:	em_estba:*
34:	em_estfun:*
35:	em_esthum1:*
36:	em_esthum2:*
37:	em_esthum3:*
38:	em_esthum4:*
39:	em_esthum5:*
40:	em_esthum6:*
41:	em_esthum7:*
42:	em_esthum8:*
43:	em_esthum9:*
44:	em_esthum10:*
45:	em_esthum11:*
46:	em_esthum12:*
47:	em_esthum13:*
48:	em_esthum14:*
49:	em_esthum15:*
50:	em_esthum16:*
51:	em_esthum17:*
52:	em_esthum18:*
53:	em_esthum19:*
54:	em_esthum20:*
55:	em_esthum21:*
56:	em_esthum22:*
57:	em_esthum23:*
58:	em_esthum24:*
59:	em_esthum25:*
60:	em_esthum26:*
61:	em_esthum27:*
62:	em_esthum28:*
63:	em_estin1:*
64:	em_estin2:*
65:	em_estin3:*
66:	em_estin4:*
67:	em_estin5:*
68:	em_estom1:*
69:	em_estom2:*
70:	em_estov1:*
71:	em_estov2:*
72:	em_estpl1:*
73:	em_estpl2:*
74:	em_estpl3:*
75:	em_estpl4:*
76:	em_estpl5:*
77:	em_estpl6:*
78:	em_estpl7:*
79:	em_estpl8:*
80:	em_estpl9:*
81:	em_estpl10:*
82:	em_estro1:*
83:	em_estro2:*
84:	em_estro3:*
85:	em_estro4:*
86:	em_estro5:*
87:	em_estro6:*
88:	em_estro7:*
89:	em_estro8:*
90:	em_estro9:*
91:	em_estro10:*
92:	em_estro11:*
93:	em_estro12:*
94:	em_estro13:*
95:	em_estro14:*
96:	em_estro15:*
97:	em_estro16:*
98:	em_estro17:*
99:	em_estro18:*
100:	em_estro19:*
101:	em_estro20:*
102:	gb_est25:*
103:	gb_est26:*
104:	gb_est27:*
105:	gb_est28:*
106:	gb_est29:*
107:	gb_est30:*
108:	gb_est31:*
109:	gb_est32:*
110:	gb_est41:*
111:	gb_est42:*
112:	gb_est43:*
113:	gb_est44:*
114:	gb_est45:*
115:	gb_est46:*
116:	gb_est47:*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est67:\*  
137: gb\_est68:\*  
138: gb\_est69:\*  
139: gb\_est70:\*  
140: gb\_est71:\*  
141: gb\_est72:\*  
142: gb\_est73:\*  
143: gb\_est74:\*  
144: gb\_est75:\*  
145: gb\_est76:\*  
146: gb\_est77:\*  
147: gb\_est78:\*  
148: gb\_est79:\*  
149: gb\_est80:\*  
150: gb\_est81:\*  
151: gb\_est82:\*  
152: gb\_est83:\*  
153: gb\_est84:\*  
154: gb\_est85:\*  
155: gb\_est86:\*  
156: gb\_est87:\*  
157: gb\_est88:\*  
158: gb\_est89:\*  
159: gb\_est90:\*  
160: gb\_est91:\*  
161: gb\_est92:\*  
162: gb\_est93:\*  
163: gb\_est94:\*  
164: gb\_est95:\*  
165: gb\_est96:\*  
166: gb\_est97:\*  
167: gb\_est98:\*  
168: gb\_est99:\*  
169: gb\_est100:\*  
170: gb\_est101:\*  
171: gb\_est102:\*  
172: gb\_est103:\*  
173: gb\_est104:\*  
174: gb\_est105:\*  
175: gb\_est106:\*  
176: gb\_est107:\*  
177: gb\_est108:\*  
178: gb\_est109:\*  
179: gb\_est110:\*  
180: gb\_est111:\*  
181: gb\_est112:\*  
182: gb\_est113:\*  
183: gb\_est114:\*  
184: gb\_est115:\*  
185: gb\_est116:\*  
186: gb\_est117:\*  
187: gb\_est118:\*  
188: gb\_est119:\*  
189: gb\_est120:\*

190: gb\_est121:\*  
191: gb\_est122:\*  
192: gb\_est123:\*  
193: gb\_est124:\*  
194: gb\_est125:\*  
195: gb\_est126:\*  
196: gb\_est127:\*  
197: gb\_est128:\*  
198: gb\_est129:\*  
199: gb\_est130:\*  
200: gb\_est131:\*  
201: gb\_est132:\*  
202: gb\_est133:\*  
203: gb\_est134:\*  
204: gb\_est135:\*  
205: gb\_est136:\*  
206: gb\_est137:\*  
207: gb\_est138:\*  
208: gb\_est139:\*  
209: gb\_est140:\*  
210: gb\_est141:\*  
211: gb\_est142:\*  
212: gb\_est143:\*  
213: gb\_est144:\*  
214: gb\_est145:\*  
215: gb\_est146:\*  
216: gb\_est147:\*  
217: gb\_est148:\*  
218: gb\_est149:\*  
219: gb\_est150:\*  
220: gb\_est151:\*  
221: gb\_est152:\*  
222: gb\_est153:\*  
223: gb\_est154:\*  
224: gb\_est155:\*  
225: gb\_est156:\*  
226: gb\_est157:\*  
227: gb\_est158:\*  
228: gb\_est159:\*  
229: gb\_est160:\*  
230: gb\_est161:\*  
231: gb\_est162:\*  
232: gb\_est163:\*  
233: gb\_est164:\*  
234: gb\_est165:\*  
235: gb\_est166:\*  
236: gb\_est167:\*  
237: gb\_est168:\*  
238: gb\_est169:\*  
239: gb\_est170:\*  
240: gb\_est171:\*  
241: gb\_est172:\*  
242: gb\_est173:\*  
243: gb\_est174:\*  
244: gb\_est175:\*  
245: gb\_est176:\*  
246: gb\_est177:\*  
247: gb\_est178:\*  
248: gb\_est179:\*  
249: gb\_est180:\*  
250: gb\_est181:\*  
251: gb\_est182:\*  
252: gb\_est183:\*  
253: gb\_est184:\*  
254: gb\_est185:\*  
255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.2	67.7	738	150	BF582153 602099743
2	211.6	65.9	949	150	BF579007 602096124
3	206	64.2	946	155	BG569760 602590367
4	205.6	64.0	434	115	AW406486 UI-HF-BL0
5	204.4	63.7	398	115	AW405309 UI-HF-BL0
6	202.8	63.2	482	32	AV733856 UI-HF-BL0
7	201.2	62.7	519	115	AW405183 AV733856
8	200.8	62.6	385	115	AW405025 UI-HF-BL0
9	199.6	62.2	468	115	AW405643 UI-HF-BL0
10	199.2	62.1	624	166	BE306691 601104076
11	198	61.7	468	115	AW404506 UI-HF-BL0
12	198	61.7	1015	155	BG536848 602566386
13	196.4	61.2	465	115	AW404697 UI-HF-BL0
14	195.4	60.9	548	155	BG568486 60257455
15	194.8	60.7	485	110	AV734882 AV734882
16	193	60.1	451	170	BF74574 IL3-EF011
17	193	60.1	758	154	BG534598 602553450
18	192	59.8	330	115	AW406212 UI-HF-BL0
19	191.6	59.7	514	115	AW405207 UI-HF-BL0
20	191.6	59.7	615	122	AW959456 EST371526
21	191.4	59.6	461	115	AW406219 UI-HF-BL0
22	191.4	59.6	849	150	BF583521 602101553
23	191.4	59.6	1061	151	BF663663 602143371
24	189.4	59.0	413	115	AW406440 UI-HF-BL0
25	189.2	58.9	656	154	BG482934 602502942
26	188.4	58.7	409	115	AW406057 UI-HF-BL0
27	187.6	58.4	639	32	AV734416 AV734416
28	186.8	58.2	443	115	AW405460 UI-HF-BL0
29	186.8	58.2	448	115	AW404726 UI-HF-BL0
30	185.8	57.9	868	155	BG539952 602567464
31	185.6	57.8	708	166	BE309445 601095331
32	185.4	57.8	317	115	AW404261 UI-HF-BL0
33	185.2	57.7	748	154	BG529887 602559987
34	185	57.6	504	115	AW405787 UI-HF-BL0
35	183.4	57.1	369	115	AW405943 UI-HF-BL0
36	182.6	56.9	833	172	BF975235 602244740
37	181.8	56.6	518	115	AW406576 UI-HF-BL0
38	181.8	56.6	644	115	AW405817 UI-HF-BL0
39	181.6	56.6	719	154	BG536027 602564303
40	181.6	56.6	895	151	BF663197 602144313
41	181.2	56.4	473	115	AW406934 UI-HF-BL0
42	180.8	56.3	1047	155	BG545546 602572793
43	180.4	56.2	425	115	AW406785 UI-HF-BL0
44	180	56.1	604	115	AW405198 UI-HF-BL0
45	179.8	56.0	408	115	AW404674 UI-HF-BL0

## ALIGNMENTS

RESULT	1
BF582153	
LOCUS	BF582153
DEFINITION	602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5', mRNA sequence.
ACCESSION	BF582153
VERSION	BF582153.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 738)
TITLE	NIH-MGC http://mgc.nci.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

FEATURES  
source

Query Match 67.7%; Score 217.2; DB 150; Length 738;  
Best Local Similarity 84.0%; Pred. No. 3.3e-56;  
Matches 267; Conservative 2; Mismatches 45; Indels 4; Gaps 2;  
QY 6 TGTGCTAACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGGACTCTTTC 65  
DB 78 TGTGCTAACTCAGTCTCCAGCCACCCCTGCTCTGACTCCAGGAGATAGCGTCACTTTC 137  
QY 66 CTGCGAGGCGAGCCAAAGTATTAGCAACCACTACACTGATATCAACAAGGCGCTGTC 125  
DB 138 CTGCGAGGCGAGCCAAAGTATTAGCAACCACTACACTGATATCAACAAGGCGCTGTC 197  
QY 126 AGCCCAAGGCTTCTCATCMKTTATCGTCCAGTCCATCTGCGGATCCCGCCAGGTT 185  
DB 198 GTCTCCAAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTGCGGATCCCGCCAGGTT 257  
QY 186 CAGTGGCAGTGGATCAGGAGACAGATTTCACCCCTACTATCTCCAGTCTGGAGCGCTGAAGA 245  
DB 258 CAGTGGCAGTGGATCAGGAGACAGATTTCACCTCTCAGTATCAACAGTGTGGAGACTGAAGA 317  
QY 246 TTTTGGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCA---CACGTTGGAGGGGG 302  
DB 318 -TTTGGAGTATTTCTGTCAACAGAGTAACAGCTGGCTGAGCTCAGCTCACGTTGGTCTGG 376  
QY 303 GACCAAGGTGGAAATTA 320  
DB 377 GACCAAGCTGGAGCTGAA 394

BASE COUNT  
ORIGIN

210 a 189 c 172 g 167 t

Email: cgabps-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9801 row: f column: 11

High quality sequence stop: 714.

Location/Qualifiers

1. .738

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:4219402"

/clone\_lib="NCI\_CGAP\_Co24"

/lab\_host="DHI08 (T1 phase-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;

Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1A09792 row: p column: 05  
High quality sequence start: 9  
High quality sequence stop: 730.

FEATURES  
source  
Location/Qualifiers  
1. .949

/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4216180"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 278 a 241 c 210 g 220 t

Query Match 65.9%; Score 211.6; DB 150; Length 949;  
Best Local Similarity 81.2%; Pred. No. 1.9e-54;  
Matches 255; Conservative 2; Mismatches 56; Indels 1; Gaps 1;

Qy 6 TGTGTAACAGCTCTCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGAGCTTTTC 65  
Dy 83 TGTACTACTCAGCTCTCAGCCACCCTGTCTGTGACTCCAGGAGATAGCGTCAGCTTTTC 142  
Qy 66 CTGCCAGGAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCTGTCA 125  
Dy 143 CTGAGGCCAGCAAAAGTATTAGCAACCACTACACTGGTATCAACAAGTACATGA 202  
Qy 126 AGCCCCAGGCTTCTATCMKKTATCGTTCCAGTCCACTCTCTGGATCCCGCCAGGTT 185  
Dy 203 GTCTCCGAGGCTTCTCATCAAGTTTGTTCCTCCAGTCCATCTCTGGATCCCGCTCCAGTT 262  
Qy 186 CAGTGGCAGTGGATCAGGACAGATTTTCACCTCAGTATCTCCAGTCTGGAGCTGAAGA 245  
Dy 263 CAGTGGCAGTGGATCAGGACAAATTTTCACTCTCAGTATCCGCACTGTGGAGACTGAAGA 322  
Qy 246 TTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTCAGCTCAGCTTCCGAGGGGGAC 305  
Dy 323 -TTTGGATGTATTCTGTCTCAGAGAGTACAGTGTGGCGGTCACTCGGTCTCTGGAC 381  
Qy 306 CAAGGTGGAAATTA 319  
Dy 382 CAAACTGGAGCTGA 395

RESULT 3  
BG569760 946 bp mRNA EST 10-APR-2001  
LOCUS 602590367F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4717049 5',  
DEFINITION mRNA sequence.  
ACCESSION BG569760  
VERSION BG569760.1 GI:13577413  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 946)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CMI566 row: e column: 18  
High quality sequence stop: 738.

FEATURES  
source  
Location/Qualifiers  
1. .946

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4717049"  
/clone\_lib="NIH\_MGC\_77"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."  
BASE COUNT 295 a 248 c 247 g 156 t

Query Match 64.2%; Score 206; DB 155; Length 946;  
Best Local Similarity 77.5%; Pred. No. 1e-52;  
Matches 248; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

Qy 1 GAGATTGTGCTAAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60  
Dy 96 GAATCTGTGTGACACAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 155  
Qy 61 CTTTCTCTCCAGGCGGCGGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120  
Dy 156 CTCCTCTCGAGGGCGAGAGTGTAGCAGCCACTTAGCCTGTGTACCAACAGAACT 215  
Qy 121 GGTCAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCACTCTCTGGATCCCGCC 180  
Dy 216 GGCCAGGCTCCAGGCTCCCTCATCTATGATGCATCCACAGGCGCACTGGCATCGCAGCC 275  
Qy 181 AGTTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTTCCACTTCTCCAGTCTGGAGCT 240  
Dy 276 AGTTTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGCAGCTAGAGCT 335  
Qy 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGCTGCAGCTGCAGAGGG 300  
Dy 336 GAAGATTTTGCAGTCTATTACTGTCAACAGTGGTAGCAACTGGGCGCTCACTTTTCGCGGA 395  
Qy 301 GGGACCAAGGTGGAAATTA 320  
Dy 396 GGGACCAAGGTGGAGATTA 415

RESULT 4  
AW406486 434 bp mRNA EST 16-FEB-2000  
LOCUS UI-HF-BLO-acr-f-12-0-UI.F1 NIH\_MGC\_37 Homo sapiens cDNA clone  
DEFINITION IMAGE:3060238 5', mRNA sequence.  
ACCESSION AW406486  
VERSION AW406486.1 GI:6925543  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 434)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.



TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.

## FEATURES

source

Location/Qualifiers

1. 434  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3060238"  
/clone\_lib="NIH\_MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: p77T3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonald, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT

99 a 127 c 106 g 102 t

ORIGIN

Query Match 64.0%; Score 205.6; DB 115; Length 434;  
Best Local Similarity 77.7%; Pred. No. 1e-52;  
Matches 247; Conservative 1; Mismatches 70; Indels 0; Gaps 0;

QY 3 GATGTGCTAAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGCGGCACT 62  
DB 7 GGTGTGTGTACAGTCTCCAGCCACCTGTCTTGTCTCCAGGGAAGAGCCACCT 66  
QY 63 TTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGCCCTGG 122  
DB 67 CTCCTGCGAGGGCGGTACAGATTAACAACTACTAGCGGTGATCAACAGAAACCTGG 126  
QY 123 TCAAGCCCAAGGCTTCTCAKMTATCGTCCAGTCCATCTCTGGGATCCCGCCAG 182  
DB 127 CCAGCTCCAGGCTCTCATCTATGATGATCAACAGGGCCATGGCATCCAGCCAG 186  
QY 183 GTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCCTGA 242  
DB 187 GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTCGAGCCTGA 246  
QY 243 AGATTTTGCAGTCTATTACTGTCAACAGTGGGAGCTGGGCTCACAGTTCGGAGGGG 302  
DB 247 AGATTTTGCAGTCTATTACTGTCAACAGTGGGAGCTGGGCTCACAGTTCGGAGGGG 306  
QY 303 GACCAAGGTGGAAATTA 320  
DB 307 GACCAAGGTGGAGATCA 324

RESULT 5

AW405309 398 bp mRNA EST 16-FEB-2000  
LOCUS UI-HF-BL0-ack-c-01-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
DEFINITION IMAGE:3059305 5', mRNA sequence.  
ACCESSION AW405309  
VERSION AW405309.1 GI:6924366  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 398)  
NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.

## FEATURES

source

Location/Qualifiers

1. 398  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3059305"  
/clone\_lib="NIH\_MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: p77T3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonald, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT

88 a 123 c 98 g 89 t

ORIGIN

Query Match 63.7%; Score 204.4; DB 115; Length 398;  
Best Local Similarity 77.2%; Pred. No. 2.4e-52;  
Matches 247; Conservative 1; Mismatches 72; Indels 0; Gaps 0;

QY 1 GAGATTGTCTAATCTCCAGCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGCGGCACT 60  
DB 44 GAAATTGTGTTACAGCTCTCCAGCCACCTGTCTTGTCTCCAGGGAAGAGCCACC 103  
QY 61 CTTTCTGCGCAGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCT 120  
DB 104 CTCCTCTGCGAGGCGAGTCAGAGTGTAGCAGCTACTTAGCTGTGATCAACAGAACT 163  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGCC 180  
DB 164 GGGCAGGCTCCAGGCTCCTCATCTCTGATGATCAACAGGGCCACTGGCATCCAGCC 223  
QY 181 AGGTTTCAGTGGCAGTGGATCAGGAGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240  
DB 224 AGGTTTCAGTGGCAGTGGGTCTGGGACAGCTTCACTCTCACCATCAGCAGCTAGAGCT 283  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGTGGCAGCTGGCCCTCACACAGGAGG 300  
DB 284 GAAGATTTTGCAGTCTATTACTGTCAACAGCTGGCAGCTGGCCCTTCGGAGG 343  
QY 301 GGGACCAAGGTGGAAATTA 320  
DB 344 GGGACCAAGGTGGAAATCA 363

RESULT 6

AW733856 482 bp mRNA EST 17-OCT-2000  
LOCUS AV733856 cda Homo sapiens cDNA clone cDABAH01 5', mRNA sequence.  
DEFINITION AV733856  
ACCESSION AV733856  
VERSION AV733856.1 GI:10851401  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE 1 (bases 1 to 385)  
 NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward.

FEATURES  
 source  
 1. .385  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3058252"  
 /clone\_lib="NIH\_MGC\_37"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LT1)"  
 /note="Vector: pT7T3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
 BASE COUNT 88 a 114 c 98 g 85 t

Query Match 62.6%; Score 200.8; DB 115; Length 385;  
 Best Local Similarity 76.7%; Pred. No. 3e-51;  
 Matches 244; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

QY 3 GATTGTCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACTCT 62  
 DB 7 GATTGTCTGACAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACTCT 66  
 QY 63 TTCTGTCAGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAGGCGCTGG 122  
 DB 67 CTCCTGCGAGGCCAGTCCAGAGTGTTCGAGCTACTTAGCCTGGTATCAACAAGAACCTGG 126  
 QY 123 TCAGCCCGAGGCTCTCATCMKKTATCGTCCAGTCCATCTCTGGATCCCGCCAG 182  
 DB 127 CCAGGCTCCAGGCTCTCATCTATGATGATCCAGAGGCCACTGGCATCCCGCCAG 186  
 QY 183 GTTCAGTGGCAGTGGATCAGGACAGATTTTACCCCTCATTCTCCAGTCTGGAGCCTGA 242  
 DB 187 GTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGCAGCTTAGAGCCTGA 246  
 QY 243 AGATTTGCGAGTCTATTACTGTCAACAGATGGGAGCTGGCCTCACAGTTCGAGGGGG 302  
 DB 247 AGATTTGCGAGTCTATTACTGTCAACAGATGGGAGCTGGCCTCACAGTTCGAGGGGG 306  
 QY 303 GACCAAGGTGGAATTA 320  
 DB 307 GACGAAGGTGGAATTA 324

RESULT 9  
 AW405643  
 LOCUS AW405643 468 bp mRNA EST 16-FEB-2000  
 DEFINITION UI-HF-BL0-abs-F-05-0-UI.r1 NIH\_MGC\_37 Homo sapiens CDNA clone  
 IMAGE:3057561 5', mRNA sequence.  
 ACCESSION AW405643  
 VERSION AW405643.1 GI:6924700  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 468)  
 NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M.B. Soares Lab  
 CDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: M13 Forward.

FEATURES  
 source  
 1. .468  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3057561"  
 /clone\_lib="NIH\_MGC\_37"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LT1)"  
 /note="Vector: pT7T3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
 BASE COUNT 110 a 137 c 115 g 106 t

Query Match 62.2%; Score 199.6; DB 115; Length 468;  
 Best Local Similarity 76.2%; Pred. No. 7.6e-51;  
 Matches 244; Conservative 1; Mismatches 75; Indels 0; Gaps 0;

QY 1 GAGATTGTCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACT 60  
 DB 23 GAAATTGTGTGACAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAGGGCGACT 82  
 QY 61 CTTCCTGCCAGGCCAGCCAAAGTATTAGCAACCCACTACACTGGTATCAACAAGGCGCT 120  
 DB 83 CTCCTCTCGAGGCCAGTCCAGAGTGTTCAGCGCTACTTAGCCTGGTATCAACAAGAACCT 142  
 QY 121 GGTCAGCCCGAGGCTCTCATCMKKTATCGTCCAGTCCATCTCTGGATCCCGCC 180  
 DB 143 GGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGAGGCCACTGGCATCCCGCC 202  
 QY 181 AGGTTTCACTGGCAGTGGATCAGGACAGATTTTACCCCTCATTCTCCAGTCTGGAGCCT 240  
 DB 203 AGGTTTCACTGGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGCAGCTAGAGCCT 262  
 QY 241 GAAGATTTGCGAGTCTATTACTGTCAACAGATGGGAGCTGGCCTCACAGCTTCGAGGG 300  
 DB 263 GAAGATTTGCGAGTCTATTACTGTCAACAGATGGGAGCTGGCCTCACAGCTTCGAGGG 322  
 QY 301 GGGACCAAGGTGGAATTA 320  
 DB 323 GGGACCAAGGTGGAATTA 342

RESULT 10  
 BE306691  
 LOCUS BE306691 624 bp mRNA EST 26-OCT-2000  
 DEFINITION 601104076f1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3501355 5',  
 mRNA sequence.  
 ACCESSION BE306691  
 VERSION BE306691.1 GI:9160297  
 KEYWORDS EST.

SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
AUTHORS 1 (bases 1 to 624)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
cDNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM8561 row: 9 column: 20  
High quality sequence stop: 598.

FEATURES  
Location/Qualifiers  
1..624  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:3501355"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
/note="Organ: lung; Vector: pCMV-Sport6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 172 a 166 c 145 g 141 t  
ORIGIN

Query Match  
Best Local Similarity 62.1%; Score 199.2; DB 166; Length 624;  
Matches 243; Conservative 2; Mismatches 75; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGCGACT 60  
DB 59 GACATCTGTATGACCCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGCGACT 60  
QY 61 CTTTCCTGCCAGGCCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCT 118  
DB 119 CTTTCCTGTAGGGCCAGCCAGATATTACAGAACCTACACTGGTATCAACAAGGCT 120  
QY 121 GGTCACGCCCAAGGCTTCTATCMKKTATCGTTCAGTCCATCTCTGGATCCCGCC 178  
DB 179 CATGGGACTCCAAGGCTTCTATCAAGTATGACCTGATCCCATCTCTGGATCCCGCC 180  
QY 181 AGTTTCAGTGGCAGTGGATCAGGAGAGTTCACCTCCTCACTATCTCCAGTCTGGAGCT 238  
DB 239 AGTTTCAGTGGCAGTGGATCAGGAGAGTTCACCTCCTCACTATCTCCAGTCTGGAGCT 240  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTCCGAGG 298  
DB 299 GAAGATGAAGGAATATATTACTGTCTTCAAGGTTACAGCATCCGCTATACGTTCCGATCG 300  
QY 301 GGGACCAAGGTGGAAATTA 320  
DB 359 GGGACCAAGGTGGAAATTA 378

RESULT 11  
AW404506 468 bp mRNA EST 16-FEB-2000  
LOCUS UT-HF-BL0-abv-a-05-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
DEFINITION IMAGE:3058065 5', mRNA sequence.  
ACCESSION AW404506  
VERSION AW404506.1 GI:6923563

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 468)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Sequencing by: M.B. Soares Lab  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.

FEATURES  
Location/Qualifiers  
1..468  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3058065"  
/clone\_lib="NIH\_MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/lab\_host="DH10B (LT1)"  
/note="Vector: pT7-Tac; Site\_1: NotI; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5Kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 106 a 137 c 114 g 111 t  
ORIGIN

Query Match  
Best Local Similarity 61.7%; Score 198; DB 115; Length 468;  
Matches 243; Conservative 1; Mismatches 76; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGCGACT 60  
DB 41 GAAATTGTGTGACACAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAGGCGACT 60  
QY 61 CTTTCCTGCCAGGCCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCT 100  
DB 101 CTCTCTGTCAGGGCCAGTCTAGAGTGTAGCAGTCTAGCTGGTACCAACAACCT 120  
QY 121 GGTCACGCCCAAGGCTTCTATCMKKTATCGTTCAGTCCATCTCTGGATCCCGCC 160  
DB 161 GGCAGGCTCCAGGCTCTCTATGATGATCAACAGGCGCCACTGGCATCCAGCC 180  
QY 181 AGTTTCAGTGGCAGTGGATCAGGAGAGTTCACCTCCTCACTATCTCCAGTCTGGAGCT 220  
DB 221 AGTTTCAGTGGCAGTGGTCTGGACAGTCTCACTCTCACCATCAGAGCTTAGAGCT 240  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTCCGAGG 280  
DB 281 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTCCGAGG 300  
QY 301 GGGACCAAGGTGGAAATTA 320  
DB 341 GGGACCAAGGTGGAGATCA 360

RESULT 12  
BG536848  
LOCUS 602566386F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4691085 5',  
DEFINITION mRNA sequence.

```

ACCESSION      BG536848
VERSION        BG536848.1  GI:13528394
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                CDNA Library Preparation: CLONTECH Laboratories, Inc.
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: L1CM1509 row: k column: 22
                High quality sequence stop: 624.
                Location/Qualifiers
                1..1015
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4691085"
                /clone_lib="NIH_MGC_77"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1;
                SfiI (ggcgctggcc); Site:2: SfiI (ggccattggcc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CAGCGCCATTATGGC-3' and 3' adaptor sequence:
                5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.9
                kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH_MGC Library."
                BASE COUNT  273 a 284 c 251 g 205 t
                ORIGIN
                Query Match      61.7%; Score 198; DB 155; Length 1015;
                Best Local Similarity 75.9%; Pred. No. 3e-50;
                Matches 243; Conservative 1; Mismatches 76; Indels 0; Gaps 0;

QY  1  GAGATTGTGCTAAGTCTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  95  GAAATTGTGTGACACAGTCTCCAGCCACCTGTCTTGTCTCCAGGAGAAAGGCGACC 154
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  61  CTTTCTCCAGGCGCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  155  CTCTCTGAGGCGCAGTGTAGCAGTACTTAGCTGTGTTACCAACAGAACCT 214
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  121  GGTCAGCCCAAGGCTTCATCMKKTATCGTTTCCAGTCCATCTCTGGATCCCGGCC 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  215  GGCCAGGCTCCAGGCTCTCATCTATGATGCATCCACAGGCGCACTGGCATCCCGACC 274
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  181  AGTTTCAAGTGGGATCAGGACAGATTTACCTCTCACTATCTCAGTCTGGAGCCT 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  275  AGTTTCAAGTGGGATCAGGACAGATTTACCTCTCACTATCTCAGTCTGGAGCCT 334
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  241  GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGAGCTGGCTTCACAGCTTCGGAGGG 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  335  GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGAGCTGGCTTCACAGCTTCGGAGGG 394
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  301  GGGACCAAGTGGAAATTA 320
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  395  GGGACCAAGTGGATATCA 414
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

FEATURES       source
                Location/Qualifiers
                1..465
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:3058518"
                /clone_lib="NIH_MGC_37"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LT1)"
                /note="Vector: pT73-Pac; Site:1: NotI; Site:2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                BASE COUNT  108 a 139 c 115 g 103 t
                ORIGIN
                Query Match      61.2%; Score 196.4; DB 115; Length 465;
                Best Local Similarity 75.6%; Pred. No. 7.4e-50;
                Matches 242; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

QY  1  GAGATTGTGCTAAGTCTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  85  GAAATAGTGTAGCAGCAGTCTCCAGCCACCTGTCTGTCTCCAGGAGAAAGGCGACC 144
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  61  CTTTCTCCAGGCGCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  145  CTCTCTGAGGCGCAGTGTAGCAGTGTAGCAACAACCTTAGCTGTGTTACCAACAGAACCT 204
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  121  GGTCAGCCCAAGGCTTCATCMKKTATCGTTTCCAGTCCATCTCTGGATCCCGGCC 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  205  GGCCAGGCTCCAGGCTCTCATCTATGTTGCATCCACAGGCGCACTGGTATCCCGACC 264
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  181  AGTTTCAAGTGGGATCAGGACAGATTTACCTCTCACTATCTCAGTCTGGAGCCT 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  265  AGTTTCAAGTGGGATCAGGACAGATTTACCTCTCACTATCTCAGTCTGGAGCCT 324
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  241  GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGAGCTGGCTTCACAGCTTCGGAGGG 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  325  GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCGAGCTGGCTTCACAGCTTCGGAGGG 384
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY  301  GGGACCAAGTGGAAATTA 320
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  385  GGGACCAAGTGGAGATCA 404
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 14  
BG568486 548 bp mRNA EST 10-APR-2001  
LOCUS 602587455F1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4716468 5',  
DEFINITION mRNA sequence.  
ACCESSION BG568486  
VERSION BG568486  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 548)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cnapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM1564 row: m column: 13  
High quality sequence stop: 548.  
FEATURES  
Location/Qualifiers  
1..548  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4716468"  
/clone\_lib="NIH\_MGC\_76"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="organ: liver; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggccgctggcc); Site\_2: SfiI (ggccattatggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGGCGGCGAGATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."  
BASE COUNT 126 a 162 c 139 g 121 t  
ORIGIN

Query Match 60.9%; Score 195.4; DB 155; Length 548;  
Best Local Similarity 75.3%; Pred. No. 1.6e-49;  
Matches 241; Conservative 1; Mismatches 77; Indels 0; Gaps 0;  
QY 1 GAGATTGCTAACTAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60  
DB 106 GAAATTGTGTGACAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60  
QY 61 CTTCCTGCGAGCCGCAAGATTATAGCAACCACTACACTGGTATCAACAAAGGCTT 120  
DB 166 CTCCTCTGAGGCGCAGTCAAGATGTGGCAGTACTTACCTGGTACCAAGAAACCT 225  
QY 121 GGTCAAGCCCAAGGCTTCTCATCKKATATCGTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 226 GCGCAGGCTCCAGGCTCTCATCTATGATAGTCCACAGGCGCCACTGGCTCCAGCC 285  
QY 181 AGTTTCAGTGGCAGTGGATTCAGGAGCAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240  
DB 286 AGTTTCAGTGGCAGTGGGCTGGGACAGACTTCACTCTCACCATCAGCAGCTAGAGCT 345  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACCTTGGAGGG 300  
DB 346 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACCTTGGAGGG 405

QY 301 GGGACCAAGGTGGAAATTA 319  
DB 406 GGGACCAAGGTGGAAATCA 424  
RESULT 15  
LOCUS AV734882 485 bp mRNA EST 17-OCT-2000  
DEFINITION AV734882 cda Homo sapiens cDNA clone cdABFC04 5', mRNA sequence.  
ACCESSION AV734882  
VERSION AV734882.1 GI:10852427  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 485)  
AUTHORS Yang, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N.,  
Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu,  
W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J.,  
Chen, Z. and Han, Z.  
TITLE Homo sapiens cDNA cda clones  
JOURNAL Unpublished (2000)  
COMMENT Contact: Zequang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.  
FEATURES  
Location/Qualifiers  
1..485  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="cdABFC04"  
/clone\_lib="cda"  
/tissue\_type="pheochromocytoma"  
/dev\_stage="Adult"  
/lab\_host="BM25.8"  
/note="vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiI"  
BASE COUNT 99 a 148 c 118 g 120 t  
ORIGIN

Query Match 60.7%; Score 194.8; DB 110; Length 485;  
Best Local Similarity 75.3%; Pred. No. 2.3e-49;  
Matches 241; Conservative 1; Mismatches 78; Indels 0; Gaps 0;  
QY 1 GAGATTGCTAACTAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60  
DB 92 GAAATTGTGTGACAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 151  
QY 61 CTTCCTGCGAGCCGCAAGATTATAGCAACCACTACACTGGTATCAACAAAGGCTT 120  
DB 152 CTTCCTGCGAGCCGCTCAGTGTAGCAGCTCTTACCTGGTACCAAGAAACCT 211  
QY 121 GGTCAAGCCCAAGGCTTCTCATCKKATATCGTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 212 GCGCAGGCTCCAGGCTCTCATCTCTGATGATCATCAACAGGCGCCCTGGCATCCACCC 271  
QY 181 AGTTTCAGTGGCAGTGGATTCAGGAGCAGATTTACCCCTCACTATCTCCAGTCTGGAGCT 240  
DB 272 AGTTTCAGTGGCAGTGGGCTGGGACAGCTTCACTCTCACCATTACAGCTTAAGCT 331  
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACCTTGGAGGG 300  
DB 332 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACCTTGGAGGG 391  
QY 301 GGGACCAAGGTGGAAATTA 320  
DB 392 GGGACCAAGGTGGAGCTCA 411

Thu Oct 11 16:16:08 2001

Search completed: October 11, 2001, 14:34:05  
Job time: 5542 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:12:39 ; Search time 177.65 seconds  
(without alignments)  
1134.570 Million cell updates/sec

Title: US-08-791-391A-31  
Perfect score: 321  
Sequence: 1 GAGATTGTGCTAACTCAGTC.....GGACCAAGTGGAATTAAG 321

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0601.\*

- 1: /SIDS1/gcgdata/geneseq/geneseq/NA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseq/NA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq/NA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseq/NA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseq/NA1984.DAT.\*
- 6: /SIDS1/gcgdata/geneseq/geneseq/NA1985.DAT.\*
- 7: /SIDS1/gcgdata/geneseq/geneseq/NA1986.DAT.\*
- 8: /SIDS1/gcgdata/geneseq/geneseq/NA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseq/NA1988.DAT.\*
- 10: /SIDS1/gcgdata/geneseq/geneseq/NA1989.DAT.\*
- 11: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseq/NA1991.DAT.\*
- 13: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT.\*
- 14: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT.\*
- 15: /SIDS1/gcgdata/geneseq/geneseq/NA1994.DAT.\*
- 16: /SIDS1/gcgdata/geneseq/geneseq/NA1995.DAT.\*
- 17: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT.\*
- 18: /SIDS1/gcgdata/geneseq/geneseq/NA1997.DAT.\*
- 19: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	319.8	99.6	321	19	AAV49843
2	318.6	99.3	321	19	AAV49821
3	318.6	99.3	321	22	AAE28176
4	318	99.1	321	22	AAE28199
5	265.8	82.8	321	19	AAV49823
6	265.8	82.8	321	22	AAE28178
7	258.4	80.5	381	21	AAZ35244
8	250.4	78.0	321	20	AAV71800
9	250.4	78.0	338	20	AAV71802
10	245.6	76.5	381	15	AAQ64167
11	245.6	76.5	381	22	AAE58747

12	239.6	74.6	5238	11	AAQ04654	Plasmid pBtl11 enc
13	239.2	74.5	324	20	AAV71798	Murine vitronectin
14	232.8	72.5	381	21	AAZ35242	Mouse anti-verotox
15	231.6	72.1	651	21	AAA44346	Human secreted exp
16	229.6	71.5	416	18	AAZ49345	CDNA encoding kapp
17	228.4	71.2	415	21	AAQ00904	Humanised antibody
18	228.4	71.2	415	21	AAQ00906	Humanised antibody
19	228	71.0	324	17	AAZ33446	EGF receptor chime
20	223.6	69.7	486	14	AAQ43245	hIL2R Ab L chain V
21	223.6	69.7	8858	20	AAZ10202	Expression vector
22	222	69.2	363	17	AAZ38510	Light chain coding
23	218.8	68.2	415	21	AAQ01262	Mouse monoclonal a
24	216.6	67.5	315	20	AAV71803	Jk gene segment.
25	216.6	67.5	315	20	AAV71805	Humanised anti-alp
26	214	66.7	321	20	AAZ10203	DNA encoding the v
27	213.6	66.5	322	15	AAQ44714	Light chain variab
28	213.6	66.5	322	20	AAZ28545	DNA encoding the v
29	209.2	65.2	321	20	AAZ10205	Human Fab clone LP
30	206	64.2	324	22	AAE29505	Anti-IL2R-beta ant
31	205.6	64.0	322	14	AAQ36615	Insert coding for
32	205.6	64.0	1395	10	AAQ90300	B-B10 MAB L chain
33	204	63.6	321	14	AAQ43243	Anti-gp54 MAB 48-1
34	204	63.6	321	19	AAV26766	L-chain V-region o
35	204	63.6	486	14	AAQ43384	Anti-human TNF-alp
36	202.8	63.2	642	20	AAZ77408	H. pylori beta-ure
37	202.4	63.1	321	21	AAA40203	CDNA encoding kapp
38	202.4	63.1	381	18	AAZ49338	CDNA encoding kapp
39	202.4	63.1	416	18	AAZ49344	CDNA encoding kapp
40	202.4	63.1	416	18	AAZ49342	Monoclonal antibody
41	201	62.6	318	14	AAQ48766	Monoclonal antibody
42	200.8	62.6	381	19	AAV12262	Anti-gp54 MAB 48-1
43	199.8	62.2	720	19	AAV26770	Plasmid pMW152-225
44	199.2	62.1	794	17	AAZ42033	Plasmid pSW202-225
45	199.2	62.1	2070	17	AAZ42035	Plasmid pSW202-225

ALIGNMENTS

RESULT 1  
AAV49843  
ID AAV49843 standard; DNA; 321 BP.  
XX  
AC AAV49843;  
XX  
XX  
DT 02-NOV-1998 (first entry)  
XX  
DE LM609 antibody light chain variable region DNA grafted fragment.  
XX  
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; ss.  
XX Mus sp.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1..321  
FT /\*tag= a  
FT /product= "LM609 grafted antibody light chain variable  
FT /region=  
FT /note= "partial sequence, no start or stop codon given"

XX  
XX LM609 antibody lig  
PN Vitaxin antibody l  
XX DNA encoding light  
XX LM609 antibody lig  
PD Antibody LM609 lig  
XX Humanised anti-ver  
PF Humanised anti-alp  
XX Vitronectin alpha-  
PR Sequence of mouse  
XX Murine CMV5 antibo  
PA

```

XX  Glaser SM, Huse WD;
XX  WPI: 1998-437472/37.
XX  P-PSDB; AAW76006.
XX  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX  integrin - and related grafted antibodies based on murine monoclonal
XX  LM609, also related nucleic acid, used to treat, prevent or diagnose
XX  angiogenesis or restenosis
XX  Claim 24; Fig 7; 129pp; English.
XX  This sequence encodes a LM609 grafted antibody variable light chain
XX  region. LM609 and the antibody vitaxin bind selectively to integrin
XX  alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand
XX  and thus block integrin-mediated signal transduction. This is useful in
XX  the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
XX  specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX  etc.). The antibodies contain non-murine framework regions so are
XX  suitable for use in humans. Enhanced types of LM609 have affinity more
XX  than 90 times greater than that of parent the parent antibody.
XX  Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
SQ
Query Match          99.6%; Score 319.8; DB 19; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.9e-91;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
    |||||||
Db  1 gagattgtctaactcagtcctcagccaccctgtctctcagccaggaagagggcgact 60
QY  61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
    |||||||
Db  61 ctttcctgcagcgccagcaagattattagcaaccactacactggtatcaacaaggcct 120
QY  121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCTCCAGTCCATCTCTGGGATCCCCGCC 180
    |||||||
Db  121 ggtcaagcccaaggcttctcatcmkktatctccagtcctatctctgggattccccgcc 180
QY  181 AGGTTTCAGTGGAGTGGATTCAGGAGCAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
    |||||||
Db  181 aggtttcagtggtgagtggttcagggagcagatttcacccctcaactatctccagtcggagcct 240
QY  241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
    |||||||
Db  241 gaagattttgcagtcctattactgtcaacagagtggcagctggccctcacacgttcggagg 300
QY  301 GGGACCAAGGTGGAATAAG 321
    |||||||
Db  301 gggaccaaggtggaaataag 321

```

## RESULT 2

```

AAV49821
ID  AAV49821 standard; DNA; 321 BP.
XX
XX  AAV49821;
XX
XX  02-NOV-1998 (first entry)
XX
XX  Vitaxin antibody light chain variable region DNA.
XX
XX  Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX  LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX  diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX  neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX  macular degeneration; osteoporosis; ss.
XX

```

```

OS  Mus sp.
XX  Key
XX  CDS
XX  Location/Qualifiers
XX  1..321
XX  /*tag=a
XX  /product="vitaxin antibody light chain variable region"
XX  /note="partial sequence, no start or stop codon given"
XX
XX  WO9833919-A2.
XX
XX  06-AUG-1998.
XX
XX  30-JAN-1998; 98WO-US01826.
XX
XX  30-JAN-1997; 97US-0791391.
XX  (IXSY-) IXSYS INC.
XX
XX  Glaser SM, Huse WD;
XX  WPI: 1998-437472/37.
XX  P-PSDB; AAW76002.
XX
XX  Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
XX  integrin - and related grafted antibodies based on murine monoclonal
XX  LM609, also related nucleic acid, used to treat, prevent or diagnose
XX  angiogenesis or restenosis
XX  Claim 6; Fig 1b; 129pp; English.
XX
XX  This sequence encodes the vitaxin antibody variable light chain region.
XX  Vitaxin and the antibody LM609 bind selectively to integrin alphaVbeta3
XX  and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
XX  block integrin-mediated signal transduction. This is useful in the
XX  treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
XX  specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX  etc.). The antibodies contain non-murine framework regions so are
XX  suitable for use in humans. Enhanced types of LM609 have affinity more
XX  than 90 times greater than that of parent the parent antibody.
XX  Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
SQ
Query Match          99.3%; Score 318.6; DB 19; Length 321;
Best Local Similarity 99.1%; Pred. No. 6.9e-91;
Matches 318; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY  1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
    |||||||
Db  1 gagattgtctaactcagtcctcagccaccctgtctctcagccaggaagagggcgact 60
QY  61 CTTTCCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120
    |||||||
Db  61 ctttcctgcagcgccagcaagattattagcaaccactacactggtatcaacaaggcct 120
QY  121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCTCCAGTCCATCTCTGGGATCCCCGCC 180
    |||||||
Db  121 ggtcaagcccaaggcttctcatcmkktatctccagtcctatctctgggattccccgcc 180
QY  181 AGGTTTCAGTGGAGTGGATTCAGGAGCAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
    |||||||
Db  181 aggtttcagtggtgagtggttcagggagcagatttcacccctcaactatctccagtcggagcct 240
QY  241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTCCGAGGG 300
    |||||||
Db  241 gaagattttgcagtcctattactgtcaacagagtggcagctggccctcacacgttcggagg 300
QY  301 GGGACCAAGGTGGAATAAG 321
    |||||||
Db  301 gggaccaaggtggaaataag 321

```

```
RESULT 3
AAF28176
ID AAF28176 standard; DNA; 321 BP.
XX
AC AAF28176;
XX
DT 03-APR-2001 (first entry)
XX
DE Vitaxin light chain variable region DNA.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX osteoporosis -
XX
XX Disclosure; Fig 1; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta_3 integrin or
XX their functional fragments. The antibodies or their functional
XX fragments can be used in the diagnosis and treatment of
XX alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX diseases (such as psoriasis and chronic articular rheumatism),
XX disorders associated with inappropriate or inopportune invasion of
XX vessels (such as diabetic retinopathy, neovascular glaucoma and
XX cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX
XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
XX
Query Match 99.3%; Score 318.6; DB 22; Length 321;
Best Local Similarity 99.1%; Pred. No. 6.9e-91;
Matches 318; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
DB 1 gagattgtctaactagttccagccacctgtctctcagccagcagagaaagggcgact 60
QY 61 CTTTCTGCCAGGCGCCAGCAAGATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
DB 61 ctttctgccaggccagcgaagattaggcaaccacctacactggtatcaacaagcgct 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCTCAGTCCATCTCTGGATCCCCGCC 180
DB 121 ggtcaagccccagggcttctcataagatcgtttccagtcctctctggtatccccgcc 180
QY 181 AGGTTCAAGTGGCAGTGATGAGGACAGATTTCACCTCTACTATCTCCAGTCTGGAGCCT 240
DB 181 aggttcagtggtgagtgatgagacagatttcacctctactatctccagtcctggagcct 240
QY 241 GAAGATTGTGCACTTATTACTGTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGAGGG 300
```

```
DB 241 gaagatttgcagtcattactgtcaacagagtgcagctggcctcacagttcggagg 300
QY 301 GGGACCAAGGTGGAATTAAG 321
DB 301 gggaccaaggtggaattaag 321
RESULT 4
AAF28199
ID AAF28199 standard; DNA; 321 BP.
XX
AC AAF28199;
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding light chain variable region of LM609.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX osteoporosis -
XX
XX Disclosure; Fig 7; 132pp; English.
XX
XX The present invention relates to enhanced LM609 grafted antibodies
XX exhibiting selective binding affinity to alphavbeta_3 integrin or
XX their functional fragments. The antibodies or their functional
XX fragments can be used in the diagnosis and treatment of
XX alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
XX diseases (such as psoriasis and chronic articular rheumatism),
XX disorders associated with inappropriate or inopportune invasion of
XX vessels (such as diabetic retinopathy, neovascular glaucoma and
XX cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX diseases (such as macular degeneration), restenosis and
XX osteoporosis.
XX
XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
XX
Query Match 99.1%; Score 318; DB 22; Length 321;
Best Local Similarity 99.1%; Pred. No. 1.1e-90;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCTGTCTCAGCCAGGAGAAAGGCGACT 60
DB 1 gagattgtctaactagttccagccacctgtctcagccagcagagaaagggcgact 60
QY 61 CTTTCTGCCAGGCGCCAGCAAGATTAGCAACACCTACACTGGTATCAACAAGGCCT 120
DB 61 ctttctgccaggccagcgaagattaggcaaccacctacactggtatcaacaagcgct 120
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCTCAGTCCATCTCTGGATCCCCGCC 180
DB 121 ggtcaagccccagggcttctcataagatcgtttccagtcctctctggtatccccgcc 180
```

Db 121 ggtcaagccccaggcttctctatcnnntatgttccccagtcacatctctggtggtcccccgc 180

Qy 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACCCCTCAGTATCCAGTCTGGAGCCT 240  
 |||||  
 Db 181 aggttcagtgagtgatcaggagacagatttcacccctcactatctccagtcgtgagcct 240  
 |||||

Qy 241 GAAGATTTGTCAGTCTATTACTGTCACACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGGG 300  
 |||||  
 Db 241 gaagattttgcagtcattactgtcaacagagtgagcagtggtgagtcggtcgcaggg 300  
 |||||

Qy 301 GGGACCAAGGTGGAAATTAAG 321  
 |||||  
 Db 301 gggaccaaggtggaattaa 321

RESULT 5  
 AAV49823  
 ID AAV49823 standard; DNA; 321 BP.  
 XX  
 AC AAV49823;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 antibody light chain variable region DNA fragment.  
 XX  
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..321  
 FT /\*tag= a  
 FT /product= "LM609 antibody light chain variable region"  
 FT /note= "partial sequence, no start or stop codon given"  
 XX  
 PN W09833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 WPI; 1998-437472/37.  
 DR P-PSDB; AAW75004.  
 DR  
 XX  
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Claim 40; Fig 2b; 129pp; English.  
 XX  
 CC This sequence encodes the LM609 antibody variable light chain region.  
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX

SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 82.8%; Score 265.8; DB 19; Length 321;  
 Best Local Similarity 88.8%; Pred. No. 2.9e-74;  
 Matches 285; Conservative 2; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GAGATTGCTGAACCTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGAGAAAGGCGGACT 60  
 |||||  
 Db 1 gatatttgtaactcagtcagtcagccacctgtctgtgacaccagagatagcgtcagt 60  
 |||||

Qy 61 CTTTCCTGCCAGGCGAGCCAAAGTATTAGCAACACCTACACTGCTATCAACAAAGGCGCT 120  
 |||||  
 Db 61 ctttctctgccagggccagccaaagtatttagcaaccacctacactgttatcaacaaatca 120  
 |||||

Qy 121 GGTCAAGCCCCCAAGGCTTCTCATCMKKTATGTTCCCTCAGTCCATCTCTGGATCCCCGCC 180  
 |||||  
 Db 121 catgagtcctccaaggtctctcatcaagtcgtgtccccagtcacatctctggtatccccctcc 180  
 |||||

Qy 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACCCCTCAGTATCCAGTCTGGAGCCT 240  
 |||||  
 Db 181 aggttcagtgagtgatcaggagacagatttcgctctcagtcatacaacagtgagagact 240  
 |||||

Qy 241 GAAGATTTGTCAGTCTATTACTGTCACACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGGG 300  
 |||||  
 Db 241 gaagattttggaatgtatttctgtcaacagagtgagcagtcggtcctcacacgcttcgaggg 300  
 |||||

Qy 301 GGGACCAAGGTGGAAATTAAG 321  
 |||||  
 Db 301 gggaccaaggtggaattaa 321

RESULT 6  
 AAF28178  
 ID AAF28178 standard; DNA; 321 BP.  
 XX  
 AC AAF28178;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Antibody LM609 light chain variable region DNA.  
 XX  
 KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 2; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC angiogenesis and treatment of  
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 82.8%; Score 265.8; DB 22; Length 321;  
 Best Local Similarity 88.8%; Pred. No. 2.9e-74;  
 Matches 285; Conservative 2; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
 |||||  
 Db 1 gatattgttaactcagttccagccacccctgtctgtgacaccagagatagcgtcagt 60  
 |||||

QY 61 CTTTCTGCGCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120  
 |||||  
 Db 61 cttctctgcccagccagccaaagtattagcaaccactacactggtatcaacaaaatca 120  
 |||||

QY 121 GGTCAAGCCCAAGGCTTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180  
 |||||  
 Db 121 catgagctctccagggctctcatcaagatcgttccagtcctctctggatccctcc 180  
 |||||

QY 181 AGGTTCAAGTGGCAGTGGTCCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
 |||||  
 Db 181 aggttcagtgccagtgatcaggagacagatttcgctcagttatcaacagtgtagact 240  
 |||||

QY 241 GAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGTCTGGAGGG 300  
 |||||  
 Db 241 gaagatttgggaatttcttctcaacagagtgccagctggcctcacacgttccggagg 300  
 |||||

QY 301 GGGACCAAGCTGGAATTAAG 321  
 |||||  
 Db 301 gggaccaagctggaaattaag 321  
 |||||

## RESULT 7

AAZ35244  
 ID AAZ35244 standard; cDNA; 381 BP.

XX AC AAZ35244;

XX 13-MAR-2000 (first entry)

XX Humanised anti-verotoxin II antibody VTml-1 VL cDNA.

XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;  
 KW monoclonal antibody; light chain; mouse; human; humanised antibody;  
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
 KW HUS; therapy; ss.

XX Homo sapiens.

OS Synthetic.

XX key Location/Qualifiers

FT sig\_peptide 1..60

FT /tag= a

FT mat\_peptide 61..381

FT /tag= b

XX WO9595629-A1.

XX 25-NOV-1999.

XX 19-MAY-1999; 99WO-US11179.

XX 20-MAY-1998; 98US-0086570.

XX (TEIJ ) TEIJIN LTD.

PA (PROT-) PROTEIN DESIGN LABS INC.

XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, CO MS, Vasques M;  
 XX WPI; 2000-086580/07.  
 DR P-PSDB; AAY32407.

XX Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli -

XX Disclosure; Fig 2b; 59pp; English.

XX This DNA sequence codes for a humanised light chain variable region  
 CC (see AAY32407) of murine monoclonal antibody VTml-1 (MuVTml-1), an  
 CC antibody that specifically binds to the B subunit of verotoxin II  
 CC (VT2). The invention relates to humanised antibodies against VT2  
 CC that are capable of neutralizing VT2 and/or VT2 variants. The  
 CC humanised antibody is a humanized form of MuVTml-1 comprising the  
 CC complementarity determining regions of MuVTml-1 (see AAY32404-05) and  
 CC heavy and light chain variable region frameworks from the human GF4  
 CC antibody heavy and light chain frameworks, provided that at least 1  
 CC position selected from L49, H29, H30, H49 and H98 is occupied by the  
 CC amino acid at the equivalent position of the MuVTml-1 antibody heavy  
 CC or light chain variable region framework. Such humanized antibodies  
 CC have an affinity for VT2 that is 3-, 5 or 10-times that of MuVTml-1.  
 CC They are used for treating a patient suffering from, or at risk of,  
 CC the toxic effects from VT2 (claimed), especially for treating  
 CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic  
 CC uraemic syndrome (HUS).

XX SQ Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;

Query Match 80.5%; Score 258.4; DB 21; Length 381;  
 Best Local Similarity 87.5%; Pred. No. 6.5e-72;  
 Matches 280; Conservative 2; Mismatches 38; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
 |||||  
 Db 61 gaaattgtctaaactcagttctccagccacctgtctgtctctccaggagaaagccact 120  
 |||||

QY 61 CTTTCTGCGCAGGCGCCAAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120  
 |||||  
 Db 121 cttctctgaggggcagtcacaaactattagcaacaactacactggtatcaacaaaacca 180  
 |||||

QY 121 GGTCAAGCCCAAGGCTTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180  
 |||||  
 Db 181 ggtcaggtccaaaggcttctcatcaaatcgtctctccagtcctctctggtatccccgcc 240  
 |||||

QY 181 AGGTTCAAGTGGCAGTGGTCCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
 |||||  
 Db 241 aggttcagtgccagtgatcaggagacagatttcactctcactatcagcagtcgtgaatct 300  
 |||||

QY 241 GAGATTTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACAGTCTGGAGGG 300  
 |||||  
 Db 301 gaagatttgcagtgattactgtcaacagagttacagtggtccgctcacgttcggtcaa 360  
 |||||

QY 301 GGGACCAAGGTGGAATTAAG 320  
 |||||

Db 361 gggaccaaggtggagatcaa 380

## RESULT 8

AAV71800

ID AAV71800 standard; cDNA; 321 BP.

XX AC AAV71800;

XX 15-MAR-1999 (first entry)

XX Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL cDNA.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
 KW D12HZHC-10; ds.

XX Homo sapiens.  
 OS Synthetic.

PN WO9840488-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX JOHANSON KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

DR P-PSDB; AAW84098.

XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis

PS Claim 2; Page 61-62; 97pp; English.

XX This DNA sequence codes for the light chain variable region (VL,  
 CC see AAW84098) of humanised anti-alpha-v beta-3 vitronectin receptor  
 CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence  
 CC (see AAW84096) of human Kabat subgroup III kappa chain, with  
 CC complementarity determining regions from the murine anti-human  
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see  
 CC AAW84094). 3 Murine framework residues (1, 49 and 60) are retained  
 CC in the synthetic VL. A humanised VH DNA sequence is also provided  
 CC (see AAW71799). Humanised antibodies of the invention can be used  
 CC for passive immunotherapy of a disorder mediated by the alpha-v  
 CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-  
 CC related disorders, such as angiogenesis associated with diabetic  
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory  
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,  
 CC e.g. solid tumour metastasis, and diseases where bone resorption is  
 CC associated with pathology such as osteoporosis, hyperparathyroidism,  
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions  
 CC produced by bone metastasis, bone loss due to immobilisation or sex  
 CC hormone deficiency. They can also be used for targeted drug  
 CC therapy, and for detection and diagnosis.

XX Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 other;

Query Match 78.0%; Score 250.4; DB 20; Length 321;  
 Best Local Similarity 85.9%; Pred. NO. 2e-69;  
 Matches 275; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGCT 60

DB 1 gacatagtactgactcagtcctccaggccacctgtcttctgtctccaggagaaagagccacc 60

QY 61 CTTTCTGTCAGCCAGCCGCAAAAGTATTAGCAACCACTTACCTGGTATCAACAAAAGGCT 120

DB 61 cttctctgagggccagccaaagattagcaaccacctacactggtatcaacaaaacct 120

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCAGTCCATCTCTGGGATCCCGGCC 180

DB 121 ggccaggtcccgcgctctctcatcaagtatgcttccagtcctatctctgggtacccctcc 180

QY 181 AGGTTTCAGTGGCAGTGATTCAGGAGCAATTCACCCCTCACTATCTCCAGTCTGGCGCT 240

XX |||||

DB 181 aggttcagtggcagtgatcaggagacagatttctactctcaccatcagcgtctagagcct 240

RESULT 9

AAV71802

XX AAV71802 standard; cDNA; 338 BP.

XX AAV71802;

XX 15-MAR-1999 (first entry)

XX Vitronectin alpha-v beta-3 MAB VL cDNA.

XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.

XX Mus sp.

OS Synthetic.

XX WO9840488-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX JOHANSON KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

DR P-PSDB; AAW84100.

XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis

XX Example 13; Page 64; 97pp; English.

XX This DNA sequence codes for the region of the murine monoclonal  
 CC antibody (MAB) D12 light chain variable region (VL, see AAW85000)  
 CC that is altered in humanised D12 VL (see also AAW84098), including  
 CC the first 5 amino acids of the human kappa constant region. It was  
 CC prepared from 4 overlapping synthetic oligonucleotides (see  
 CC AAV71816-19). The synthetic gene was used to construct an expression  
 CC vector for humanised D12 VL. D12 is an anti-alpha-v beta-3  
 CC vitronectin receptor MAB. Humanised D12 MABs can be used for  
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3  
 CC vitronectin receptor, e.g. restenosis and angiogenic associated  
 CC diseases.

XX Sequence 338 BP; 82 A; 99 C; 79 G; 78 T; 0 other;

Query Match 78.0%; Score 250.4; DB 20; Length 338;

Best Local Similarity 85.9%; Pred. NO. 2.1e-69;

Matches 275; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGCT 60







PN WO9840488-A1.  
 XX 17-SEP-1998.  
 XX 12-MAR-1998; 98WO-US04987.  
 XX 12-MAR-1997; 97US-0039609.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX Johanson KO, Jonak ZL, Taylor AH;  
 XX WPI; 1999-034590/03.  
 DR P-PSDB; AAW84094.  
 XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis  
 XX Example 13; Page 59-60; 97pp; English.  
 XX This cDNA sequence codes for the light chain variable region (VL,  
 CC see AAW84094) of the anti-human alpha-v beta-3 vitronectin receptor  
 CC murine monoclonal antibody D12. It was obtained from hybridoma  
 CC total RNA by RT-PCR using mouse kappa and N-terminal-based primers  
 CC (see AAV71808-09). A heavy chain variable region clone (see AAV71797)  
 CC has also been identified. D12 VH and VL show sequence similarity  
 CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see  
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see  
 CC AAW84098) were constructed by combining the framework regions of the  
 CC human V region consensus sequences with complementarity determining  
 CC regions of D12 (keeping some preferred murine framework residues).  
 CC The humanised antibodies are specifically reactive with the human  
 CC alpha-v beta-3 protein receptor and capable of neutralising the  
 CC receptor. They can be used for passive immunotherapy of a disorder  
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular  
 CC disorders or angiogenic-related disorders, such as angiogenesis  
 CC associated with diabetic retinopathy, atherosclerosis and  
 CC restenosis, chronic inflammatory disorders, macular degeneration,  
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and  
 CC diseases where bone resorption is associated with pathology such as  
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia  
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone  
 CC loss due to immobilisation or sex hormone deficiency. They can also  
 CC be used for targeted drug therapy, and for detection and diagnosis.  
 XX Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;  
 SQ

Query Match 74.5%; Score 239.2; DB 20; Length 324;  
 Best Local Similarity 83.88; Pred. No. 6.8e-66;  
 Matches 268; Conservative 2; Mismatches 50; Indels 0; Gaps 0;  
 QY 1 GAGATTGTGCTAAGTCTCCAGCCACCGCTGTCTCAGCCGAGGAGGCGGACT 60  
 DB 1 gacattgtctgactcagtcctccagccacctgtctgtactccagagatagcgtcagt 60  
 QY 61 CTTTCCTGCGCAGCGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGCCCT 120  
 DB 61 ctttcctgcagggccagcagaagtattagcaaccacacctacactgggtatcaacaagaatca 120  
 QY 121 GGTCACAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGGCC 180  
 DB 121 catgagctccaagcttctcataagtagcttcccagtcactctctggatccccctcc 180  
 QY 181 AGGTTACGTAGTCAGTATGAGGACAGATTTACCTCTACTATCTCAGTCTCGAGGCT 240  
 DB 181 aggttcagagcagtgatcagggacagatttctactctcaatcatcaacattttggagact 240  
 QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCTCAGACGTTTCGGAGGG 300  
 DB 241 gaggatttggagatgtatttctgtcaacagagtaacagctggccttccacgttcggtctgc 300

QY 301 GGGACCAAGGTGGAATTAA 320  
 DB 301 gggacaaacttggaaataaa 320  
 RESULT 14  
 AAZ35242  
 ID AAZ35242 standard; cDNA; 381 BP.  
 XX AAZ35242;  
 XX 13-MAR-2000 (first entry)  
 XX Mouse anti-verotoxin II antibody VTml-1 VL CDNA.  
 XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;  
 KW monoclonal antibody; light chain; mouse; humanised antibody;  
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
 KW HUS; therapy; ss.  
 XX Mus musculus.  
 XX Key Location/Qualifiers  
 FT sig\_peptide 1..60  
 FT mat\_peptide 58..381  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /transl\_except= (pos:184..186, aa:Lys)  
 XX WO9959629-A1.  
 XX 25-NOV-1999.  
 XX 19-MAY-1999; 99WO-US11179.  
 XX 20-MAY-1998; 98US-0086570.  
 XX (TEIJ ) TEIJIN LTD.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;  
 DR WPI; 2000-086580/07.  
 DR P-PSDB; AAY32405.  
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli -  
 XX Disclosure; Fig 1b; 59pp; English.  
 XX This DNA sequence codes for the light chain variable region (see  
 CC AAY32405) of murine monoclonal antibody VTml-1 (MuVTml-1), an  
 CC antibody that specifically binds to the B subunit of verotoxin II  
 CC (VT2). The invention relates to humanised antibodies against VT2  
 CC that are capable of neutralizing VT2 and/or VT2 variants. The  
 CC humanised antibody is a humanized form of MuVTml-1 comprising the  
 CC complementarity determining regions of MuVTml-1 and heavy and  
 CC light chain variable region frameworks from the human G4 antibody  
 CC heavy and light chain frameworks, provided that at least 1 position  
 CC selected from L49, H29, H30, H49 and H98 is occupied by the amino  
 CC acid at the equivalent position of the MuVTml-1 antibody heavy or  
 CC light chain variable region framework. Such humanized antibodies  
 CC (see AAY32405-07) have an affinity for VT2 that is 3-, 5 or 10-times  
 CC that of MuVTml-1. They are used for treating a patient suffering  
 CC from, or at risk of, the toxic effects from VT2 (claimed), especially  
 CC for treating verotoxin producing Escherichia coli (VTEC) infection,  
 CC and haemolytic uraemic syndrome (HUS).  
 XX Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;  
 SQ

Query Match 72.5%; Score 232.8; DB 21; Length 381;

Best Local Similarity 82.5%; Pred. No. 7.4e-64;  
Matches 264; Conservative 2; Mismatches 54; Indels 0; Gaps 0;

QY 1 GAGATTGCTGTAAGTCTCAGTCCAGCCACCCTCTCTCAGCCAGGAGAAAGGGCGACT 60  
DB 61 gatgtgtgtaactcagtcctcagccaccctgtgtgactccagagatagcgtcagt 120  
QY 61 CTTCCTGCGCAGCCGACCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120  
DB 121 cttctcagggcagtcagtaactattagcaaacactacactgggtatcaacaaatca 180  
QY 121 GGTCAAGCCCAAGGTTCTCATCTCMKKTATCGTTCACAGTCCATCTCTGGATCCCGCC 180  
DB 181 catgagctcacaaggtctctcacaagtcgtctccagtcctcctggtggtccctcc 240  
QY 181 AGCTTCAGTGGCAGTGGATGAGGAGAGATTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
DB 241 aggttcagtgggcagtgatcagggagagatttcactctcagtcacacagtgtygaaact 300  
QY 241 GAAGATTTCGACGTCTATTACTGTCAACAGAGTGGCGCTCACAGTTCGGAGGG 300  
DB 301 gaagatttggaaatgattctgtcaacagagttacagctggcgctcagcttcggtgct 360  
QY 301 GGCACCAAGTGAATATA 320  
DB 361 gggaccaagctggagctgaa 380

RESULT 15  
AAA44346  
ID AAA44346 standard; cDNA; 651 BP.  
XX  
AC AAA44346;  
DT 21-AUG-2000 (first entry)  
XX  
DE Human secreted expressed sequence tag SEQ ID NO:921.  
XX  
KW Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;  
KW expressed sequence tag; EST; probe; chemotactic; proliferative;  
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;  
KW antitumor; antineoplastic; cytostatic; antibacterial; antifungal;  
KW antiviral; antidiabetic; antiasthmatic; vulnary; antiparkinsonian;  
KW antitumor; osteopathic; neuroprotective; nontropic; antiparkinsonian;  
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;  
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;  
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;  
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;  
KW central nervous system disorder; Alzheimer's disease; stroke;  
KW Parkinson's disease; Huntington's disease; coagulation disorder;  
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;  
KW tumour; infection; depression; psoriasis; ss.  
XX  
OS Homo sapiens.

XX  
PN WO200021991-A1.  
XX  
PD 20-APR-2000.  
XX  
PF 15-OCT-1999; 99WO-US24206.  
XX  
PR 15-OCT-1998; 98US-0104436.  
XX  
PA (GEMY ) GENETICS INST INC.  
XX  
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Bowman MR;  
XX  
DR WPI; 2000-317938/27.  
XX  
PT Isolated polynucleotides, and encoded proteins, comprising secreted  
PT expressed sequence tags (SESTs), useful for treating various disorders -  
PT such as autoimmune, infectious, and central nervous system disorders -

XX  
PS  
XX  
CC AAA3426 to AAA5025 represent specifically claimed secreted expressed  
CC sequence tags (SESTs), isolated from human, mouse, chicken and rat  
CC tissue sources. The SESTs can have a range of activities depending on  
CC the tissues they were isolated from. The activities include:  
CC chemotactic; proliferative; immunomodulatory; haematopoietic;  
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;  
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;  
CC antiasthmatic; vulnary; antitumor; osteopathic; neuroprotective;  
CC nontropic; antiparkinsonian; antipsoriatic; cerebroprotective;  
CC anticonvulsant; and antidepressant. The SESTs can be used for gene  
CC therapy and in vaccines. The SESTs are useful as probes for the  
CC identification and isolation of full-length cDNAs and genomic DNA  
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs  
CC are useful in assays for determining biological activity and raising  
CC antibodies. They may be useful for treatment of autoimmune disorders  
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,  
CC osteoporosis, osteoarthritis, central nervous system disorders  
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's  
CC disease), tumours, bacterial, fungal or viral infections, depression and  
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 651 BP; 174 A; 166 C; 151 G; 160 T; 0 other;

Query Match 72.1%; Score 231.6; DB 21; Length 651;  
Best Local Similarity 82.5%; Pred. No. 2.2e-63;  
Matches 264; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY 1 GAGATTGCTGTAAGTCTCAGTCCAGCCACCCTCTCTCAGCCAGGAGAAAGGGCGACT 60  
DB 94 gacattgtgactcagtcctcagccaccctgtgtgactccagagatagctct 153  
QY 61 CTTCCTGCGCAGCCGACCAAGTATTAGCAACACCTACACTGGTATCAACAAGGCCT 120  
DB 154 cttctcagggcagtcagtcagagatttagcagacttactacactgggtatcaacaaatca 213  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCACAGTCCATCTCTGGATCCCGCC 180  
DB 214 catgagctcacaaggtctctcacaatagcttcccaatcctctctggatccctcc 273  
QY 181 AGTTCAGTGGCAGTGGATGAGGAGAGATTCACCCCTCACTATCTCCAGTCTGGAGCCT 240  
DB 274 aggttcagtgagtgatcaggttcagatttcactctcagtcacacagtgtygaaact 333  
QY 241 GAAGATTTCGACGTCTATTACTGTCAACAGAGTGGCGCTCACAGTTCGGAGGG 300  
DB 334 gaagatgttggagtgattactgtcaaaaatggtccagcttctccgtacacgcttcggaggg 393  
QY 301 GGCACCAAGTGAATATA 320  
DB 394 gggaccaagctggagctgaa 413

Search completed: October 11, 2001, 15:12:40  
Job time: 6472 sec

---

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2001, 15:14:15 ; Search time 87.94 seconds  
(without alignments)  
691.027 Million cell updates/sec

Title: US-08-791-391A-31

Perfect score: 321

Sequence: 1 GAGATTGCTCACTACGTC.....GGACCAAGGTGGAATTAAG 321

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.6	76.5	381	1	US-07-634-278-82
2	245.6	76.5	381	1	US-08-477-728-82
3	245.6	76.5	381	1	US-08-474-040-82
4	245.6	76.5	381	1	US-08-487-200-82
5	245.6	76.5	381	4	US-08-484-537-82
6	245.6	76.5	424	1	US-08-436-463-3
7	239.6	74.6	5238	6	5453363-1
8	224.8	70.0	321	2	US-08-232-081B-35
9	223.6	69.7	321	2	US-08-232-081B-36
10	222	69.2	324	2	US-08-737-560A-13
11	222	69.2	363	2	US-08-737-560A-8
12	213.6	66.5	322	2	US-08-476-176B-3
13	213.6	66.5	322	3	US-08-127-721A-3
14	213.6	66.5	322	3	US-08-485-246A-3
15	204	63.6	321	2	US-08-232-081B-39
16	201	62.6	318	1	US-08-326-362-3
17	198.8	61.9	318	2	US-08-800-198-3
18	198.8	61.9	318	3	US-09-296-595-3
19	198.8	61.9	720	2	US-08-800-198-7
20	198.8	61.9	720	3	US-09-296-595-7
21	198	61.7	720	2	US-07-956-399-1
22	193.8	60.4	429	2	US-08-653-402B-7
23	191.2	59.6	321	1	US-08-192-102-2
24	191.2	59.6	321	1	US-08-324-799-2
25	191.2	59.6	321	2	US-08-192-661A-2
26	191.2	59.6	717	2	US-07-956-399-3
27	187.2	58.3	812	1	US-08-053-131-178

28	187.2	58.3	812	1	US-08-096-762-178
29	187.2	58.3	812	4	US-09-042-353-41
30	180.8	56.3	900	1	US-08-053-131-180
31	180.8	56.3	900	1	US-08-096-762-180
32	180.8	56.3	900	4	US-09-042-353-43
33	180.8	56.2	931	3	US-09-049-672A-19
34	176.4	55.0	642	2	US-08-480-753-5
35	176.4	55.0	642	3	US-09-041-889-10
36	176.4	55.0	642	3	US-08-837-058-10
37	174.4	54.3	321	4	US-09-240-274-201
38	173.8	54.1	325	5	PCT-US93-12501-1
39	172	53.6	424	2	US-08-476-176B-9
40	172	53.6	424	3	US-08-127-721A-9
41	172	53.6	424	3	US-08-485-246A-9
42	171.8	53.5	321	4	US-09-240-274-216
43	171.2	53.3	321	4	US-09-240-274-107
44	170.8	53.2	321	3	US-08-783-853A-43
45	170.4	53.1	424	2	US-08-476-176B-7

## ALIGNMENTS

RESULT 1  
US-07-634-278-82  
; Sequence 82, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

```
;
;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381.
;
; US-07-634-278-82

Query Match
Best Local Similarity 76.5%; Score 245.6; DB 1; Length 381;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
Db 61 GATATTGTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 120
QY 61 CTTTCCTGCCAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 121 CTTTCCTGCCAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCTCCAGTCCATCTCTGGGATCCCGCC 180
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATCTCCAGTCCATCTCTGGGATCCCGCC 240
QY 181 AGTTTCAGTGGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 241 AGTTTCAGTGGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 241 GAAGATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 301 GAAGATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 301 GGGACCAAGTGGAAATAA 320
Db 361 GGGACCAAGTGGAAATAA 380

RESULT 2
US-08-477-728-82
; Sequence 82, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
;
; US-08-477-728-82

Query Match
Best Local Similarity 76.5%; Score 245.6; DB 1; Length 381;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
Db 61 GATATTGTGCTCACTCACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 120
QY 61 CTTTCCTGCCAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 121 CTTTCCTGCCAGCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCTCCAGTCCATCTCTGGGATCCCGCC 180
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATCTCCAGTCCATCTCTGGGATCCCGCC 240
QY 181 AGTTTCAGTGGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 241 AGTTTCAGTGGCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 241 GAAGATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 301 GAAGATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 301 GGGACCAAGTGGAAATAA 320
Db 361 GGGACCAAGTGGAAATAA 380

RESULT 3
US-08-474-040-82
; Sequence 82, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
; OS-08-474-040-82

```

Query Match	76.5%;	Score 245.6;	DB 1;	Length 381;
Best Local Similarity	85.0%;	Pred. No. 5.9e-70;		
Matches	272;	Conservative	2;	Mismatches 46; Indels 0; Gaps
QY	1	GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCCTCTCAGCCCCAGGAGAAAGGGCGACT	60	
Db	61	GATATTGTCTAACTCAGTCTCCAGCCACCCCTGTCGTGACTCCGGAGATACGCTCAGT	120	
QY	61	CTTTCTCTCGCAGGCCAGCCAAAGATTATGACCAACCACTACACTGGTGATCAACAAAGGCGCT	120	
Db	121	CTTTCTCTCGCAGGCCAGCCAAAGATTATGACCAACCACTACACTGGTGATCAACAAAGTCA	180	
QY	121	GGTCAAGCCCCAAGGGCTTCTCATCMKKKTATCGTTCCTCAGTCCCATCTCTGGGATCCCCGGC	180	
Db	181	CATGAGTCTCCAAGGGTTCATCAAGTATGCTTCCCACTCCATCTCTGGGATCCCCGCC	240	
QY	181	AGSTTCAGTGGCAGTGGATCAGGGACAGATTTTCACCCCTCACTATCTCCAGTCTGGAGCGCT	240	
Db	241	AGSTTCAGTGGCAGTGGATCAGGGACAGATTTTCACCTCTCAGTGTCAACGGTGTGGAGACT	300	
QY	241	GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCCTCACACGTTTCGGAGGG	300	
Db	301	GAAGATTTTGGAAATGTATTTCGTCAACAGAGTAACAGTTGGCCCTCATACGTTTCGGAGGG	360	
QY	301	GGACCAAGGTGGAAATTA	320	
Db	361	GGGACCAAGCTGGAAATAAA	380	

RESULT 4  
US-08-487-200-82  
; Sequence 82, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.

```

; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
US-08-487-200-82

Query Match          76.5%; Score 245.6; DB 1; Length
Best Local Similarity 85.0%; Pred. No. 5.9e-70;
Matches 272; Conservative

QY      1   GAGATTGTGCTAACTAGTCTCAGCGCACCCCTGCTCTCAGCCGACGAGGAGGATCA
DB      61   GATATTGTGCTAACTAGTCTCAGCGCACCCCTGCTCTGACTCCGGGAG
QY      61   CTTTCCTGCCAGGCAGCCCAAAGTATTAGCAACACCCTACACTGGTGATCATC
DB      121  CTTTCCTGCAGGGCCAGCCCAAAGTATTAGCAACAACCTACACTGGTATCTG
QY      121  GGTCAGAGCCCCAAGGGCTTCATCMKMTATCGTTCCAGTCCCATCTCTCTG
DB      181  CATGAGTCTCCAAGGCTTCTCATCAAGTATGCTTCCAGTCCCATCTCTG
QY      181  AGGTTCA GTGGCAGTGGATCAGGCAGACAGATTTCACCOCTCACTATCTCCAG

```

Db 241 AGGTTGAGTGGAGTGCAGGACAGATTTCACTCTCAGTGTCAACGGTGTGGAGACT 300  
QY 241 GAAGATTTTTCAGCTATTACTCTCAACAGAGTGGCGCTCACAGCTTCGAGGG 300  
Db 301 GAGATTTTGAATGTATTCTCTCAACAGAGTAACAGTTGGCTCATAGCTTCGAGGG 360  
QY 301 GGGACCAAGGTGGAATTA 320  
Db 361 GGGACCAAGGTGGAATTA 380

RESULT 5  
US-08-484-537-82  
; Sequence 82, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381

US-08-484-537-82

Query Match 76.5%; Score 245.6; DB 4; Length 381;  
Best Local Similarity 85.0%; Pred. No. 5.9e-70;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;  
QY 1 GAGATTGCTCTACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGAGCT 60  
Db 61 GATATTGCTCTACTCAGTCTCCAGCCACCCCTGTCTGTGACTCCGGGAGATAGCGTCAGT 120  
QY 61 CTTTCTCGCAGGCCAGCCAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120  
Db 121 CTTTCTCGCAGGCCAGCCAAAGTATTAGCAACAACCTACACTGGTATCAACAATAATCA 180  
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGGCC 180  
Db 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCTCC 240  
QY 181 AGTTTCAGTGGCAGTGATCAGGACAGATTTCAACCTCAGTCTCCAGTCTGGAGGCT 240  
Db 241 AGTTTCAGTGGCAGTGATCAGGACAGATTTCAACCTCAGTCTCCAGTCTGGAGGCT 300  
QY 241 GAAGATTTTTCAGTCTATTACTGTCAACAGAGTGGCGCTCACAGCTTCGAGGG 300  
Db 301 GAAGATTTTTCAGTCTATTACTGTCAACAGAGTAAACAGTTGGCTCATAGCTTCGAGGG 360  
QY 301 GGGACCAAGGTGGAATTA 320  
Db 361 GGGACCAAGGTGGAATTA 380

RESULT 6  
US-08-436-463-3  
; Sequence 3, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-EPHILINE HERPES VIRUS-1 RECOMBINANT  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:



NAME/KEY: CDS  
LOCATION: 23...403  
US-08-436-463-3

Query Match 76.5%; Score 245.6; DB 1; Length 424;  
Best Local Similarity 85.0%; Pred. No. 6.2e-70;  
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCACCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 83 GATATTGCTAACTCAGTCTCCAGCACCCTGCTGTGACTCCAGGAGATAGCGTCAGT 142  
QY 61 CTTTCCTGCCAGGCGAGCAAGATATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
DB 143 CTTTCCTGCCAGGCGAGCAAGATATTAGCAACAACCTACACTGGTATCAACAATCA 202  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKTYATGTTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 203 CATGAGTCTCCAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 262  
QY 181 AGGTTTCAGTGCAGTGCAGGACAGATTTACACCTCTCACTATCTCCAGTCTGGAGCCT 240  
DB 263 AGGTTTCAGTGCAGTGCAGGACAGATTTACCTCTCAGTATCAACAGTGTGGAGACT 322  
QY 241 GAAGATTTTCAGTCTTATTACTGTCAACAGAGTGGCCTGCGCTCACAGTTCGGAGGG 300  
DB 323 GAAGATTTGGAATGATTTCTGTCAACAGATTAACAGTGGCCTCACAGTTCGGTGTCT 382  
QY 301 GGGACCAAGTGGAAATTA 320  
DB 383 GGGACCAAGTGGAGTGA 402

RESULT 7

5453363-1  
PATENT No. 5453363  
APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF  
TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PAT OR  
ING AROUND GENETIC EXPRESSION IN PROKARYOTES  
NUMBER OF SEQUENCES: 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206,044  
FILING DATE: 02-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 942,370  
FILING DATE: 09-SEP-1992  
APPLICATION NUMBER: 498,500  
FILING DATE: 23-MAR-1990  
APPLICATION NUMBER: 76,207  
FILING DATE: 23-OCT-1986  
SEQ ID NO: 1  
LENGTH: 5238

Query Match 74.6%; Score 239.6; DB 6; Length 5238;  
Best Local Similarity 84.1%; Pred. No. 1.5e-67;  
Matches 269; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCACCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 7 gatattgtctaactcagttccagccacctgtctgtgactccaagagatagcgtcagt 66  
QY 61 CTTTCCTGCCAGGCGAGCAAGATATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
DB 67 ctttcctgcagggcgagcaaaagtattagcaaacacctacactggtatcaacaaaatca 126  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKTYATGTTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 127 catgagctccaagggctctcatcaaatatgcttccagtcctcatctctggtatccccctct 186  
QY 181 AGGTTTCAGTGCAGTGCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

DB 187 aggttcagtgccagtgagtcagggacagattttcactctcagtatcaacagtgtagact 246  
QY 241 GAAGATTTTCAGTCTTATTACTGTCAACAGAGTGGCAGCTGGCTCAACAGTTCGGAGGG 300  
DB 247 gaagattttggaatgtatttctgtcaacagagtaacagctggcctctcacgttcggtgct 306  
QY 301 GGGACCAAGTGGAAATTA 320  
DB 307 gggaccaagctggagctgaa 326

RESULT 8

US-08-232-081B-35  
Sequence 35, Application US/08232081B  
Patent No. 5886152  
GENERAL INFORMATION:  
APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIJENES, JOHN  
APPLICANT: NOGUCHI, HIROSHI  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.081B  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-232-081B-35

Query Match 70.0%; Score 224.8; DB 2; Length 321;  
Best Local Similarity 80.9%; Pred. No. 2.7e-63;  
Matches 259; Conservative 2; Mismatches 59; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCACCCTGCTCTCAGCCAGGAGAAAGGCGACT 60  
DB 1 GAGATCGTCCTGACTCAGTCTCCAGGCACACTGCTCTGAGTCCAGGAGAAAGGCCACA 60  
QY 61 CTTTCCTGCCAGGCGAGCAAGATATTAGCAACACCTACACTGGTATCAACAAGGCGCT 120  
DB 61 CTGCTCTGCAGGGCGAGTCCAGCACCATTGGCACAAGCATACACTGGTATCAGCAGAGACCA 120  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKTYATGTTCCAGTCCATCTCTGGGATCCCGCC 180  
DB 121 GCCAGGCGCCCAAGGCTTCTCATAAAGTATGCTTCTGAGTCTATCTCTGGCATCCCTGAT 180  
QY 181 AGGTTTCAGTGCAGTGCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240

Db 181 AGTTTGGAGTGGATCAGGACAGATTTTACTCTTACAAATCTCCAGGCTGGAGCCA 240  
QY 241 GAAGATTTTGGAGTGGATCAGGACAGATTTTACTCTTACAAATCTCCAGGCTGGAGG 300  
Db 241 GAAGATTTTGGAGTGGATCAGGACAGATTTTACTCTTACAAATCTCCAGGCTGGAGG 300  
QY 301 GGGACCAAGGTGGAATAA 320  
Db 301 GGGACCAAGGTGGAATAA 320

RESULT 9  
US-08-232-081B-36  
; Sequence 36, Application US/08232081B  
; Patent No. 5886152  
; GENERAL INFORMATION:  
; APPLICANT: NAKATANI, TOMOYUKI  
; APPLICANT: GOMI, HIDEYUKI  
; APPLICANT: WIJDNES, JOHN  
; APPLICANT: NOGUCHI, HIROSHI  
; TITLE OF INVENTION: HUMANIZED B-B10  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,081B  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 20-3484  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 321 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-232-081B-36

Query Match 69.7%; Score 223.6; DB 2; Length 321;  
Best Local Similarity 80.9%; Pred. No. 6.5e-63;  
Matches 259; Conservative 1; Mismatches 60; Indels 0; Gaps 0;  
QY 1 GAGATTTGCTTACTTACTTCTCAGGACCCCTCTCTCAGCCAGGAGAAAGGGGACT 60  
Db 1 GAGATTTGCTTACTTACTTCTCAGGACCCCTCTCTCAGCCAGGAGAAAGGGGACT 60  
QY 61 CTCTTCTGCGAGGCGCAAGTATTAGCAACCACTTACCTGCTATCAACAAAGGCT 120  
Db 61 CTGCTCTGCGAGGCGCAGTACAGACCTTGGCAACATACATCTGTTATCAGCAGACCA 120  
QY 121 GTCAAGCCCCAAGGCTTCTATCMTKKTATCTGTTCCCACTCCATCTCTGGGATCCCGCC 180  
Db 121 GCGCAGGCCCCAAGGCTTCTATATATTATGCTTCTGAGTCTATCTCTGGCATCCCTGAT 180  
QY 181 AGTTTCACTGGGATCGGATCAGGACAGATTTTCAACCTCACTATCTCCAGTCTGGAGCCT 240

Db 181 AGTTTGGAGTGGATCAGGACAGATTTTACTCTTACAAATCTCCAGGCTGGAGCCA 240  
QY 241 GAAGATTTTGGAGTGGATCAGGACAGATTTTACTCTTACAAATCTCCAGGCTGGAGG 300  
Db 241 GAAGATTTTGGAGTGGATCAGGACAGATTTTACTCTTACAAATCTCCAGGCTGGAGG 300  
QY 301 GGGACCAAGGTGGAATAA 320  
Db 301 GGGACCAAGGTGGAATAA 320

RESULT 10  
US-08-737-560A-13  
; Sequence 13, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuul  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuul  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; CITY: Kwanak-gu  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1  
; OTHER INFORMATION: light chain variable region  
US-08-737-560A-13

Query Match 69.2%; Score 222; DB 2; Length 324;  
Best Local Similarity 80.6%; Pred. No. 2.1e-62;  
Matches 258; Conservative 1; Mismatches 61; Indels 0; Gaps 0;  
QY 1 GAGATTTGCTTACTTACTTCTCAGGACCCCTCTCTCAGCCAGGAGAAAGGGGACT 60

Db 1 GACATTGTGATGACCCAGCTCTCCAGCCACCAGTCTGTGACTCCAGGAGATAGAGTCTCT 60  
QY 61 CTTTCTCCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120  
Db 61 CTTTCTCCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180  
Db 121 CATGAGTCTCAAGGCTTCTCATCAATATGCTTCCCAATCACTCTGGGATCCCGCTCC 180  
QY 181 AGGTTCAAGTGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGG 240  
Db 181 AGGTTCAAGTGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGG 240  
QY 241 GAGATTTTGCAGTCTATTACTGTCAACAGAGTGGGATGGGATGGGATGGGATGGGATGGG 300  
Db 241 GAGATTTTGCAGTCTATTACTGTCAACAGAGTGGGATGGGATGGGATGGGATGGGATGGG 300  
QY 301 GGCACCAAGGTGGAATCAA 320  
Db 301 GGCACCAAGGTGGAATCAA 320

## RESULT 11

US-08-737-560A-8  
; Sequence 8, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuil  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuil  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; STREET: Kwanak-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 363 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain  
; OTHER INFORMATION: variable region  
; OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1  
; OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2  
; OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3  
; OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region  
US-08-737-560A-8

Query Match 69.2%; Score 222; DB 2; Length 363;  
Best Local Similarity 80.6%; Pred. No. 2.2e-62;  
Matches 258; Conservative 1; Mismatches 61; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCGAGGAGAGGCGGACT 60  
Db 1 GACATTGTGATGACCCAGCTCTCCAGCCACCAGTCTGTGACTCCAGGAGATAGAGTCTCT 60  
QY 61 CTTTCTCCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120  
Db 61 CTTTCTCCAGGCGCCAGCAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120  
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180  
Db 121 CATGAGTCTCAAGGCTTCTCATCAATATGCTTCCCAATCACTCTCTGGGATCCCGCTCC 180  
QY 181 AGGTTCAAGTGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGG 240  
Db 181 AGGTTCAAGTGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGG 240  
QY 241 GAGATTTTGCAGTCTATTACTGTCAACAGAGTGGGATGGGATGGGATGGGATGGGATGGG 300  
Db 241 GAGATTTTGCAGTCTATTACTGTCAACAGAGTGGGATGGGATGGGATGGGATGGGATGGG 300  
QY 301 GGCACCAAGGTGGAATCAA 320  
Db 301 GGCACCAAGGTGGAATCAA 320

## RESULT 12

US-08-476-176B-3  
; Sequence 3, Application US/08476176B  
; Patent No. 5958708  
; GENERAL INFORMATION:  
; APPLICANT: Hardman, No. 5958708man  
; APPLICANT: Kolbinger, Frank  
; APPLICANT: Saldanha, Jose  
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
; TITLE OF INVENTION: Immunoglobulin isotype  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nq. 5958708artis Patent Department  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07936-1080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,176B  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/127,721  
; FILING DATE: 27-SEPTEMBER-1993  
; APPLICATION NUMBER: US 07/952,802  
; FILING DATE: 25-SEPTEMBER-1992  
; ATTORNEY/AGENT INFORMATION:





Job time: 5003 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:02:36 ; Search time 31.63 Seconds  
(without alignments)  
257.688 Million cell updates/sec

Title: US-08-791-391a-32

Perfect score: 557

Sequence: 1 EIVLQSPATLSLSPGERAT.....COQSGSWPHTFGGKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	84.4	144	2 PL0106	Ig kappa chain pre
2	460	82.6	111	2 S23628	Ig kappa chain v r
3	458	82.2	128	2 A56701	Ig kappa chain v r
4	457	82.0	128	2 S40379	Ig kappa chain v-j
5	452.5	81.2	114	2 S54905	Ig kappa chain v r
6	451	81.0	108	2 G44151	Ig kappa chain v r
7	447	80.3	106	2 PC4282	Ig kappa chain (an
8	447	80.3	107	2 B45722	anti-glycoprotein
9	444	79.7	117	2 S40362	Ig kappa chain - h
10	443	79.5	125	2 S40344	Ig kappa chain v-j
11	442	79.4	123	2 S35479	Ig kappa chain pre
12	441	79.2	107	2 A45722	anti-glycoprotein
13	440.5	79.1	109	2 A30608	Ig kappa chain v-i
14	440	79.0	129	2 S29627	Ig kappa chain v r
15	438	78.6	128	2 S40345	Ig kappa chain v-j
16	437	78.5	107	2 S34005	Ig kappa chain v r
17	436	78.3	106	2 PL0267	Ig kappa chain v r
18	433.5	77.8	108	2 B30608	Ig kappa chain v-i
19	433.5	77.8	129	2 A32274	Ig kappa chain pre
20	432.5	77.6	109	2 G30607	Ig kappa chain v-i
21	431.5	77.5	109	1 K3HUTI	Ig kappa chain v-j
22	431	77.4	107	2 S57444	Ig kappa chain v-j
23	430.5	77.3	109	2 D30601	Ig kappa chain v-i
24	430.5	77.3	109	2 C30601	Ig kappa chain v-i
25	429.5	77.1	109	2 H30601	Ig kappa chain v-i
26	429	77.0	128	2 S40343	Ig kappa chain v-j
27	428.5	76.9	109	1 K3HUSI	Ig kappa chain v-i
28	427.5	76.8	109	2 G30601	Ig kappa chain v-i
29	427.5	76.8	109	2 B30601	Ig kappa chain v-i

30 427.5 76.8 128 2 S20636 Ig kappa chain v r  
31 427.5 76.8 129 1 K3HUAH Ig kappa chain pre  
32 426.5 76.6 215 2 JE0244 Ig kappa chain NIG  
33 425.5 76.4 108 2 C30608 Ig kappa chain v-i  
34 424.5 76.2 110 2 S20635 anti-sm antibody v  
35 424.5 76.2 129 2 S49532 Ig kappa chain v r  
36 423.5 76.0 109 2 PH0963 Ig kappa chain v-i  
37 423.5 76.0 109 2 F30607 Ig kappa chain v-i  
38 422.5 75.9 109 1 K3HWWL Ig kappa chain v-i  
39 422.5 75.9 129 1 K3HUTI Ig kappa chain pre  
40 420 75.4 114 2 S46375 Ig kappa chain v-j  
41 419.5 75.3 130 2 S40360 Ig kappa chain - h  
42 419 75.2 138 2 A26471 Ig kappa chain pre  
43 417.5 75.0 43 F30601 Ig kappa chain v-i  
44 417.5 75.0 129 2 S46369 IG light chain var  
45 417.5 75.0 134 2 S38643 Ig kappa chain v r

#### ALIGNMENTS

RESULT 1

PL0106

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C:Accession: PL0106

R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A:Reference number: PL0106; MUID:89235583

A:Accession: PL0106

A:Molecule type: mRNA

A:Residues: 1-144 <SIL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match 84.4%; Score 470; DB 2; Length 144;

Best Local Similarity 85.0%; Pred. No. 1.4e-34;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSQASQSIHNLHWYQORPGQAPRLLIYRSQTSIGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSQASQSVSYLAWYQORPGQAPRLLIYRSQTSIGIPA 80

Qy 61 RFSGSGGTDFTLTISSLEPEFAVYCCQSGSWPHTFGGKTRVEIK 107

Db 81 RFSGSGGTDFTLTISSLEPEFAVYCCQSGSWPHTFGGKTRVEIK 127

RESULT 2

S23628

Ig kappa chain v region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S23628

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A:Reference number: S23623; MUID:92156804

A:Accession: S23628

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 <OLE>





QY 64 GSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 107  
|||||  
Db 63 GSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 106

## RESULT 7

PC4282  
Ig kappa chain (anti-ss-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 21-Jan-2000  
R:Suzuki, H.; Takemura, H.; Sekine, Y.; Kashiwagi, H.  
Biochem. Biophys. Res. Commun. 232, 101-106, 1997  
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin  
A:Reference number: PC4279; MUID:97236289  
A:Accession: PC4282  
A:Molecule type: protein  
A:Residues: 1-106 <SUZ>  
A:Note: E-42  
A:Molecule type: protein  
A:Accession: PC4284  
A:Residues: 1-106 <SUZ>  
A:Note: E-56  
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjog  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 447; DB 2; Length 106;  
Best Local Similarity 81.0%; Pred. No. 1.1e-32;  
Matches 85; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 3 VLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIYXSQISGIPARF 62  
|||||  
Db 1 VLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIYDISKRATGIPAKF 60

QY 63 SSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 107  
|||||  
Db 61 SSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 105

## RESULT 8

B45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
A:Reference number: A45722; MUID:93100833  
A:Accession: B45722  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBP:120590)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 447; DB 2; Length 107;  
Best Local Similarity 75.7%; Pred. No. 1.1e-32;  
Matches 81; Conservative 17; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIYXSQISGIPA 60  
:|||||  
Db 1 DIVLTQSPATLSVTPGDVSLSCRASQISNHLHWYQOKSHESPRLLIKYASQISGIPS 60

QY 61 RFSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 107  
|||||  
Db 61 RFSGSGTDTLTINSVETEDFGVFCQQTNSWPHTFGGKLEIK 107

## RESULT 9

S40362  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40362  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40362  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-117 <KLE>  
A:Cross-references: EMBL:X72472; NID:9441412; PID:9441413  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 444; DB 2; Length 117;  
Best Local Similarity 79.4%; Pred. No. 2.2e-32;  
Matches 85; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIYXSQISGIPA 60  
|||||  
Db 11 EIVLTQSPATLSVSPGERATLSCASQSVSNLAWYQOKPGQAPRLLIYGASTRATGIPA 70

QY 61 RFSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 107  
|||||  
Db 71 RFSGSGTDTLTISLEPEFAVYVCOQYNNWPLTFGGGKVEIK 117

## RESULT 10

S40344

Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40344  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40344  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72454; NID:9441376; PIDN:CAA51122.1; PID:9441377  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 443; DB 2; Length 125;  
Best Local Similarity 81.9%; Pred. No. 2.8e-32;  
Matches 86; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSISNHLHWYQORPGQAPRLLIYXSQISGIPA 60  
:|||||  
Db 21 EVLVTQSPATLSLSPGERATLSCASQSVSTYLAWYQIQGAPRLLIYDASNRATGIPA 80

QY 61 RFSGSGTDTLTISLEPEFAVYVCOQSGSWPHTFGGKVEIK 105  
|||||  
Db 81 RFSGSGTDTLTISLEPEFAVYVCOQSRWPLTFGGGKVEIK 125

## RESULT 11

S35479

Ig kappa chain precursor V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: S35479  
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.  
Nucleic Acids Res. 20, 4099, 1992  
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m  
A:Reference number: S35479; MUID:92375706  
A:Accession: S35479  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-123 <TAK>  
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148  
C:Genetics:  
A:Map position: 6  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 442; DB 2; Length 123;  
Best Local Similarity 74.8%; Pred. No. 3.4e-32;  
Matches 80; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60  
Db 13 DIVLTQSPATLSVTPGDKVSLSCRASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPS 72  
QY 61 RFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWPHTFGGKVEIK 107  
Db 73 RFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWPHTFGGKVEIK 119

RESULT 12  
AA5722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: AA5722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
A:Reference number: AA5722; MUID:93100833  
A:Accession: AA5722  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 441; DB 2; Length 107;  
Best Local Similarity 73.8%; Pred. No. 3.6e-32;  
Matches 79; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60  
Db 1 DIVLTQSPATLSVTPGDSVSLSCRASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPS 60

QY 61 RFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWPHTFGGKVEIK 107  
Db 61 RFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWPHTFGGKVEIK 107

RESULT 13  
A30608  
Ig kappa chain V-III region (Son) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
C:Accession: A30608  
R:Goni, F.R.; Chen, P.P.; McCinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold  
J. Immunol. 142, 3158-3163, 1989

A:Title: Structural and idiotypic characterization of the L chains of human IgM autoa  
A:Reference number: A30601; MUID:89215279  
A:Accession: A30608  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 440.5; DB 2; Length 109;  
Best Local Similarity 81.5%; Pred. No. 4.1e-32;  
Matches 88; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 59  
Db 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 60

QY 60 ARFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWPHTFGGKVEIK 107  
Db 61 NRFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWPHTFGGKVEIK 108

RESULT 14  
S29627  
Ig kappa chain V region (60.3 hybridoma) - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34110; S29627

R:Walls, M.A.; Hsiao, K.; Harris, L.J.  
Nucleic Acids Res. 21, 2921-2929, 1993  
A:Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains  
A:Reference number: S34110; MUID:93324379

A:Accession: S34110  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <WAS>

A:Cross-references: EMBL:Z17330; NID:38511; PIDN:CAA78978.1; PID:g938512  
A:Note: human sequences cloned and sequenced prior to expression in mouse myeloma cel  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
C:Genetics:  
A:Insertions: 17/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 440; DB 2; Length 129;  
Best Local Similarity 79.8%; Pred. No. 5.3e-32;  
Matches 87; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCAQSQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIPA 80

QY 61 RFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWP--HTFGGKVEIK 107  
Db 81 RFSGSGSGTDFTLTISLSPEDFAVYVCOQSGSWP--HTFGGKVEIK 129

RESULT 15  
S40345  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40345

R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40345

A:Status: preliminary; translation not shown

A:Molecule type: mRNA  
A:Residues: 1-128 <KLE>  
A:Cross-references: EMBL:X72455; NID:g441378; PIDN:CAA51123.1; PID:g441379  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 438; DB 2; Length 128;  
Best Local Similarity 78.9%; Pred. No. 7.9e-32;  
Matches 86; Conservative 8; Mismatches 13; Indels 2; Gaps 1;  
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQISGIPA 60  
Db 17 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQISGIPA 60  
QY 61 RFGSGSGTDFTLTISLEPEDFAVYVCQSGSWPH--TFGGGKVEIK 107  
Db 77 RFGSGSGTDFTLTISLEPEDFAVYVCQSGSWPH--TFGGGKVEIK 125

Search completed: October 11, 2001, 12:02:36  
Job time: 301 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:08:43 ; Search time 17.83 Seconds  
(without alignments)  
205.571 Million cell updates/sec

Title: US-08-791-391A-32

Perfect score: 557

Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQSGSWPHTFGGTRKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	431.5	77.5	109	1 KV3D_HUMAN	P01622 homo sapien
2	428.5	76.9	109	1 KV3B_HUMAN	P01620 homo sapien
3	427.5	76.8	129	1 KV3L_HUMAN	P18135 homo sapien
4	427.5	75.9	109	1 KV3E_HUMAN	P01623 homo sapien
5	422.5	75.9	129	1 KV3M_HUMAN	P18136 homo sapien
6	418.5	75.1	129	1 KV3H_HUMAN	P04207 homo sapien
7	413	74.1	115	1 KV3I_HUMAN	P04433 homo sapien
8	410.5	73.7	109	1 KV3F_HUMAN	P01624 homo sapien
9	406.5	73.0	108	1 KV3A_HUMAN	P01619 homo sapien
10	406	72.9	128	1 KV3K_HUMAN	P06311 homo sapien
11	402.5	72.3	109	1 KV3G_HUMAN	P04206 homo sapien
12	380	68.2	108	1 KV1M_HUMAN	P01605 homo sapien
13	373	67.0	108	1 KV1H_HUMAN	P01600 homo sapien
14	371	66.6	111	1 KV3H_MOUSE	P01660 mus musculus
15	370	66.4	108	1 KV1Y_HUMAN	P03062 homo sapien
16	370	66.4	111	1 KV3L_MOUSE	P01664 mus musculus
17	370	66.4	111	1 KV3R_MOUSE	P01670 mus musculus
18	367.5	66.0	116	1 KV3J_HUMAN	P04434 homo sapien
19	367	65.9	129	1 KV1W_HUMAN	P04431 homo sapien
20	366	65.7	108	1 KV1E_HUMAN	P01597 homo sapien
21	365.5	65.6	100	1 KV3C_HUMAN	P01621 homo sapien
22	365	65.5	108	1 KV1P_HUMAN	P01608 homo sapien
23	365	65.5	108	1 KV1V_HUMAN	P04430 homo sapien
24	365	65.5	115	1 KV5I_MOUSE	P01642 mus musculus
25	365	65.5	134	1 KV4C_HUMAN	P06314 homo sapien
26	364.5	65.4	133	1 KV4B_HUMAN	P06313 homo sapien
27	364	65.4	111	1 KV3J_MOUSE	P01662 mus musculus
28	364	65.4	111	1 KV3T_MOUSE	P01672 mus musculus
29	364	65.4	114	1 KV4A_HUMAN	P01625 homo sapien
30	363	65.2	111	1 KV3U_MOUSE	P01673 mus musculus
31	362	65.0	108	1 KV1G_HUMAN	P01599 homo sapien
32	361	64.8	111	1 KV3M_MOUSE	P01665 mus musculus
33	360	64.6	108	1 KV1N_HUMAN	P01606 homo sapien

#### ALIGNMENTS

##### RESULT 1

```
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3)-MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01895; K3HUTI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
```

Query Match 77.5%; Score 431.5; DB 1; Length 109;  
Best Local Similarity 80.6%; Pred. No. 3.2e-38;  
Matches 87; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSQASQISN-HLHWQQRPQGPAPRLIYXSQSIGTP 59  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 EIVLTQSPCTLSLSPGERATLSQASQSVNSFLAWYQKPGAPRLIYVASSRATGTP 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 60 ARFSGSGGSDTFTLTISSLEPEDFAVYCCQSGSWPHTFGGTRKVEIK 107  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 DRFSGSGGSDTFTLTISRLEPEDFAVYCCQYQSGSPSTFGQTKVELK 108  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

##### RESULT 2

```
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 RL group.";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 CC GLOBULIN ACTIVITY.  
 DR PIR; A01892; K3HUSI.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89  
 FT NON\_TER 109 109  
 FT SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;  
 SQ  
 Query Match 76.9%; Score 428.5; DB 1; Length 109;  
 Best Local Similarity 79.8%; Pred. No. 6.6e-38;  
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQORPGQAPRLLIYRSQSISGIP 59  
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVNSYLANWYQKPGQAPRLLIYGASRRATGIP 60  
 QY 60 ARFSGSGSGTDFLTITSLRLEPEDFAVYCYQSGSWPHTFGGKVEIK 107  
 Db 61 DRFSGSGSGTDFLTITSLRLEPEDFAVYCYQSGSPQTGQGSKVEIK 108  
 RESULT 3  
 KV3L\_HUMAN STANDARD; PRT; 129 AA.  
 ID KV3L\_HUMAN  
 AC P18135;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88171307; PubMed=3127527;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene  
 RT expressed in chronic lymphocytic leukemia with little or no somatic  
 RT mutation. Implications for etiology and immunotherapy.";  
 RL J. Exp. Med. 167:840-852(1988).  
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
 CC LEUKEMIA.  
 DR PIR; P10022; K3H0HA.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.  
 FT DOMAIN 21 43 FRAMEWORK 1.  
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 56 70 FRAMEWORK 2.  
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 78 109 FRAMEWORK 3.  
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 119 129 JKI SEGMENT.  
 FT DISULFID 43 109  
 BY SIMILARITY.

FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;  
 Query Match 76.8%; Score 427.5; DB 1; Length 129;  
 Best Local Similarity 79.6%; Pred. No. 1e-37;  
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGQAPRLLIYRSQSISGIP 59  
 Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLANWYQKPGQAPRLLIYGASRRATGIP 80  
 QY 60 ARFSGSGSGTDFLTITSLRLEPEDFAVYCYQSGSWPHTFGGKVEIK 107  
 Db 81 DRFSGSGSGTDFLTITSLRLEPEDFAVYCYQSGTSPRTFGGKVEIK 128  
 RESULT 4  
 KV3E\_HUMAN STANDARD; PRT; 109 AA.  
 ID KV3E\_HUMAN  
 AC P01623;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION WOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 RL group.";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 CC GLOBULIN ACTIVITY.  
 DR PIR; A01896; K3H0WL.  
 DR HSSP; P01789; 2MCP.  
 DR InterPro; IPR003006; -.  
 DR Pfam; PF00047; Ig; 1.  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89  
 FT NON\_TER 109 109  
 FT SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;  
 SQ  
 Query Match 75.9%; Score 422.5; DB 1; Length 109;  
 Best Local Similarity 79.6%; Pred. No. 2.8e-37;  
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;  
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQORPGQAPRLLIYRSQSISGIP 59  
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLANWYQKPGQAPRLLIYGASRRATGIP 60  
 QY 60 ARFSGSGSGTDFLTITSLRLEPEDFAVYCYQSGSWPHTFGGKVEIK 107  
 Db 61 DRFSGSGSGTDFLTITSLRLEPEDFAVYCYQSGSLGRTFGGKVEIK 108  
 RESULT 5  
 KV3M\_HUMAN STANDARD; PRT; 129 AA.  
 ID KV3M\_HUMAN  
 AC P18136;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RJ J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; PLO021; K3HUHI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 75.9%; Score 422.5; DB 1; Length 129;
Best Local Similarity 79.6%; Pred. No. 3.4e-37;
Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPQAPRLLIYRSQSISGIP 59
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYGASSRATGIP 80
Qy 60 ARFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSWPHFTGGTKVEIK 107
Db 81 DRFGSGSGTDFTLTISLLEPEDFAVYVYCOQYQYVFWTGGTKVEIK 128

RESULT 6
KV3H_HUMAN STANDARD; PRT; 129 AA.
ID KV3H_HUMAN
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DE 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CIL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorce J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RJ Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

DR EMBL; M12740; AAA58992.1; -.
DR PIR; A01898; K3HUC1.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 5C13B411BE60CC14 CRC64;

Query Match 75.1%; Score 418.5; DB 1; Length 129;
Best Local Similarity 75.9%; Pred. No. 8.7e-37;
Matches 82; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPQAPRLLIYRSQSISGIPA 60
Db 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQPPRLIYGASTRATGIPA 80
Qy 61 RFSGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSW-PHTFGGTKVEIK 107
Db 81 RFSGSGSGTEFTLTISRLQSEDFAVYVYCOQYNNWPPWTFGGTRVEIK 128

RESULT 7
KV3I_HUMAN STANDARD; PRT; 115 AA.
ID KV3I_HUMAN
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DE 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.";
RJ Nucleic Acids Res. 12:9229-9236(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01568; -. NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 76 108 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(1)
RN SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3HUB6.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 73.0%; Score 406.5; DB 1; Length 108;
Best/Local Similarity 73.1%; Pred. No. 1.3e-35;
Matches 79; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 EVLTQSPATLSLSPGERATLSCQASQIS-NHLHWYQRPQAPRLLIYRSQSISGIP 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 ZVLVTSPGTLSPGZRAALSCRASQSLSGNYLAWYQKPGQAPRLMLYGVSSRATGIP 60

QY 60 ARFSGSGSGTDFLTITSSLPEDFANVYVYCOQSGSWPHTFGGKPKVEIK 107
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 DRFSGSGSGADFTLTISRLPEDFANVYVYCOQYSGSPFTFGGSKLEIK 108

RESULT 10
KV3K_HUMAN STANDARD; PRT; 128 AA.
ID KV3K_HUMAN
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(1)
SEQUENCE FROM N.A.
MEDLINE=86041852; PubMed=2997711;
RX Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
IG KAPPA CHAIN V-III REGION IARC/BL41.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.

```



```
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.9%; Score 406; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 1.7e-35;
Matches 80; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQTSIGIPA 60
DB 21 EIVLTQSPGTLSPGESATLSQASQVSSNLAQYQKRGQSPRLLIYRSQTSIGIPA 80
QY 61 RFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 81 RFGSGSGTDFTLTISLLEPEDFAVYVYCOQSTSPYTFGGKLEIK 127

RESULT 11
KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the wa idiocyptic group, in part predicted by its
RT reactivity with antipeptide antibodies."
RL Mol. Immunol. 23:239-244(1986).
DR PIR: A01893; K3HUGO.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
DR Immunoglobulin V region.
KW DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA; 11630 MW; 9349A5BID93568B6 CRC64;

Query Match 72.3%; Score 402.5; DB 1; Length 109;
Best Local Similarity 75.9%; Pred. No. 3.3e-35;
Matches 82; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQTSIGIP 59
DB 1 EIVLTQSPGTLSPGERATLSQAAALSSRGYLAQYQKPGQAPRLLIYRSQTSIGIP 60
QY 60 ARFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 61 DRFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSPRSFGGKVEIK 108

RESULT 12
KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 72.9%; Score 406; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 1.7e-35;
Matches 80; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQTSIGIPA 60
DB 21 EIVLTQSPGTLSPGESATLSQASQVSSNLAQYQKRGQSPRLLIYRSQTSIGIPA 80
QY 61 RFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 81 RFGSGSGTDFTLTISLLEPEDFAVYVYCOQSTSPYTFGGKLEIK 127

RESULT 11
KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the wa idiocyptic group, in part predicted by its
RT reactivity with antipeptide antibodies."
RL Mol. Immunol. 23:239-244(1986).
DR PIR: A01893; K3HUGO.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
DR Immunoglobulin V region.
KW DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA; 11630 MW; 9349A5BID93568B6 CRC64;

Query Match 72.3%; Score 402.5; DB 1; Length 109;
Best Local Similarity 75.9%; Pred. No. 3.3e-35;
Matches 82; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQTSIGIP 59
DB 1 EIVLTQSPGTLSPGERATLSQAAALSSRGYLAQYQKPGQAPRLLIYRSQTSIGIP 60
QY 60 ARFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 61 DRFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSPRSFGGKVEIK 108

RESULT 12
KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX NCBI_TaxID=9606;
RN SEQUENCE.
RP MEDLINE=77038198; PubMed=824717;
RX Capra J.D., Klapper D.G.;
RA "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; K1HULY.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK 1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 50 56 FRAMEWORK 2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 89 97 FRAMEWORK 3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 FRAMEWORK 4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 68.2%; Score 380; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 7.1e-33;
Matches 68; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQTSIGIPA 60
DB 1 DIQMTQSPSSLSVSGVDRTVTCQASQNVNAYLNWYQKPKGLPKLLIYGASTREAGVPS 60
QY 61 RFGSGSGTDFTLTISLLEPEDFAVYVYCOQSGSWPHTFGGKVEIK 107
DB 61 RFGSGSGTDFTLTISLLOPEDIAITYCOQYNNWPPTEFGGKVEIK 107

RESULT 13
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RA "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01868; K1HULU.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
```

Qy	57	GIPARFSGSGGDTFTLTITSSLEPEDFAVYVCQQSGSWPHTFGGTKVEIK	107
Db		:   :         :             :	
Db	61	GIPARFSGSGRDTFTLTINPVEDADVATYVCQQSNEPDYTFGGTKLEIK	111
RESULT	15		
KVLY_HUMAN		STANDARD; PRT: 108 AA.	
ID	P80362;		
AC			
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-I REGION WAT.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).		
RX	MEDLINE=95086080; PubMed=7993911;		
RA	Huang D.-B., Chang C.-H., Ainsworth C.; Bruenger A.T., Eulitz M.,		
RA	Solomon A., Stevens F.J., Schisler M.,		
RT	"Comparison of crystal structures of two homologous proteins:		
RT	structural origin of altered domain interactions in immunoglobulin		
RT	light-chain dimers."		
RN	Biochemistry 33:14848-14857(1994).		
RN	[2]		
RP	SEQUENCE OF 1-35.		
RX	MEDLINE=81267384; PubMed=6167731;		
RA	Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,		
RA	Popp R.A., Solomon A.;		
RT	"Characterization and preliminary crystallographic data on the VL-		
RT	related fragment of the human kappa Bence Jones protein Wat.";		
RJ	J. Mol. Biol. 147:185-193(1981).		
CC	-I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.		
DR	PDB; IWTU; 01-NOV-94.		
DR	InterPro; IP0003006; -.		
DR	Fam; PR00047; ig 1.		
KW	Immunoglobulin v region; Bence-Jones protein; 3D-structure.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 38		
FT	CONFLICT 30 31		
FT	NON_TER 108 108		
SO	SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;		
Query Match 66.4%; Score 370; DB 1; Length 108;			
Best Local Similarity 63.6%; Pred. No. 7.7e-32;			
Matches 68; Conservative 21; Mismatches 18; Indels 0; Gaps			
Qy	1	EIVLTQSPATLSLPGERATLSQAQSISNHLHWYQORCPQLRLIYXRYSQISIPA	60
Db		: :       : :       : :       : :       : :       : :       :	
Db	1	DIQTQSPSLNSVGDRVITICRASQDITYNVNFQORCPQKPVLIYGASILETGVS	60
Qy	61	RFGSGSGGDTFTLTITSSLEPEDFAVYVCQQSGSWPHTFGGTKVEIK	107
Db		:	
Db	61	RFGSGSGGDTFTLTITSSLEPIDIATYVCQDYDTPLFLFGGTVKDIIK	107

Search completed: October 11, 2001, 12:08:43  
Job time: 403 sec



**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	429.5	77.1	109	4	Q9UL85	Q9UL85 homo sapien	
2	428	76.8	108	4	Q9UL83	Q9UL83 homo sapien	
3	427.5	76.8	109	4	Q9UL78	Q9UL78 homo sapien	
4	402.5	72.3	109	4	Q9UL86	Q9UL86 homo sapien	
5	385	69.1	108	4	Q9UL77	Q9UL77 homo sapien	
6	372	66.8	108	4	Q9UL79	Q9UL79 homo sapien	
7	366	65.7	108	4	Q9UL70	Q9UL70 homo sapien	
8	362.5	65.1	107	4	Q9UL81	Q9UL81 homo sapien	
9	338.5	60.8	106	5	Q9UL10	Q9UL10 schistosoma	
10	334	60.0	99	11	Q9UL74	Q9UL74 mus musculus	
11	334	60.0	107	11	Q9UL84	Q9UL84 mus musculus	
12	332	59.6	298	11	Q9QYF0	Q9QYF0 mus musculus	
13	331	59.4	214	11	Q9RLA5	Q9RLA5 mus musculus	
14	326	58.5	101	11	Q9JL78	Q9JL78 mus musculus	
15	315	56.6	107	11	Q9ERZ9	Q9ERZ9 mus musculus	
16	314	56.4	103	11	Q9JL80	Q9JL80 mus musculus	
17	309	55.5	97	11	Q9JL76	Q9JL76 mus musculus	
18	309	55.5	114	4	Q9UL80	Q9UL80 homo sapien	
19	307.5	55.2	104	11	Q9JL82	Q9JL82 mus musculus	



01-MAY-2000 (TREMBlrel. 13, Created)  
 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 Homo sapiens (Human).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=98277139; PubMed=9614934;  
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 Young D.C.;  
 "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 Clin. Immunol. Immunopathol. 87:184-192(1998).  
 -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 DOMAIN.  
 EMBL; AF035037; AAD56273.1; -.  
 HSP; P01607; IREI.  
 InterPro; IPR003006; -.  
 InterPro; IPR003596; -.  
 Pfam; PF00047; Ig; 1.  
 SMART; SM00406; IGV; 1.  
 NON\_TER 1  
 NON\_TER 108  
 SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 69.1%; Score 385; DB 4; Length 108;  
 Best Local Similarity 69.2%; Pred. No. 7e-36;  
 Matches 74; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQGPAPRLIIXYSQISGIPA 60  
 Db 1 DIQMTQSPSSLSASVGRVITICRASQISLSYLNWYQKPKAPNLLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITISLPEPEFVAVYCOQSGSWPHTFGGKVEIK 107  
 Db 61 RFGSGSGTDFLTITISLQPEFVAVYCOQSYSTWTFEGGKVEIK 107

## RESULT 6

Q9UL79 ID Q9UL79 PRELIMINARY; PRT; 108 AA.  
 AC Q9UL79;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 DOMAIN.  
 DR EMBL; AF035035; AAD56271.1; -.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; -.  
 DR InterPro; IPR003596; -.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR NON\_TER 1  
 DR NON\_TER 108  
 SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 66.8%; Score 372; DB 4; Length 108;  
 Best Local Similarity 67.3%; Pred. No. 2e-34; 21; Indels 0; Gaps 0;  
 Matches 72; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQGPAPRLIIXYSQISGIPA 60  
 Db 1 DIVMTQSPSLASASTGDRVTISCRMSQGISNYLAWYQKPKAPPELLIYAASLTQSGVPS 60

Qy 61 RFGSGSGTDFLTITISLPEPEFVAVYCOQSGSWPHTFGGKVEIK 107  
 Db 61 RFGSGSGTDFLTITISLQPEFVAVYCOQYYSFPPTFGGKVEIK 107

## RESULT 7

Q9UL70 ID Q9UL70 PRELIMINARY; PRT; 108 AA.  
 AC Q9UL70;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 Clin. Immunol. Immunopathol. 87:184-192(1998).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 DOMAIN.  
 DR EMBL; AF035044; AAD56280.1; -.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; -.  
 DR InterPro; IPR003596; -.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR NON\_TER 1  
 DR NON\_TER 108  
 SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 65.7%; Score 366; DB 4; Length 108;  
 Best Local Similarity 64.5%; Pred. No. 9.5e-34;  
 Matches 69; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQGPAPRLIIXYSQISGIPA 60  
 Db 1 DIQMTQSPSSLSASVGRVITICRASQGISNYLAWYQKPKAPKSLIYAASLTQSGVPS 60

Qy 61 RFGSGSGTDFLTITISLPEPEFVAVYCOQSGSWPHTFGGKVEIK 107  
 Db 61 RFGSGSGTDFLTITISLQPEFVAVYCOQKYNAPRTFGGKLEIK 107

## RESULT 8

Q9UL81 ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
 AC Q9UL81;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;





```
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match          60.0%; Score 334; DB 11; Length 107;
Best Local Similarity 58.9%; Pred. No. 3.7e-30;
Matches 63; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQSISGIPA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSTSSLSASIGDVRXXKCSASQGISNXXWFOQKPGDGTVKLLIYTSLSXGVP 60

Qy 61 RFSGSGCTDFTLTISSEPEDFAVVYCOQSGSWPHTFGGKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGXDYSLTISNLEPEDIAITYCOQYSKFPWTFGGGKLEIK 107

RESULT 12
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CN 8 SCFV.
CN 8
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinozawa N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinozawa N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
DR EMBL: AB036341; BAA88633.1; -.
DR HSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR SMART: SM00407; Ig; 2.
DR Pfam: PF00047; Ig; 2.
DR NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=A.Ca;
RA Maikael S., Liao L., Cunningham M.W., Diamond B.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
DR EMBL: AF206028; AAF69326.1; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;

Query Match          59.6%; Score 332; DB 11; Length 298;
Best Local Similarity 57.0%; Pred. No. 2e-29;
Matches 61; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQSISGIPA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 DIETQSPASLSASVGETVTITCRASGNIHNLAWYQKQKSPOLLVNAKTLADGVP 232

Qy 61 RFSGSGCTDFTLTISSEPEDFAVVYCOQSGSWPHTFGGKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 233 RFSGSGSTQYSLKINSIQPEDFGYQCFHWFTTPTFGGKLEIK 279

RESULT 13
Q9RIA5 PRELIMINARY; PRT; 214 AA.
ID Q9RIA5
AC Q9RIA5
```

```
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RL "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; -.
DR InterPro: IPR003600; -.
DR Pfam: PF00047; Ig; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SMART: SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match          59.4%; Score 331; DB 11; Length 214;
Best Local Similarity 55.1%; Pred. No. 1.8e-29;
Matches 59; Conservative 25; Mismatches 23; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQAPRLLIYRSQSISGIPA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSFQKPGKSPKTLIYRANRLVDGVP 60

Qy 61 RFSGSGSGTDFTLTISSEPEDFAVVYCOQSGSWPHTFGGKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGQDYSLTISSEYEDMGYICLYDEFFFTFGSGTKLEIK 107

RESULT 14
Q9JL78 PRELIMINARY; PRT; 101 AA.
AC Q9JL78
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=A.Ca;
RA Maikael S., Liao L., Cunningham M.W., Diamond B.;
RL "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
DR EMBL: AF206028; AAF69326.1; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;

Query Match          58.5%; Score 326; DB 11; Length 101;
Best Local Similarity 62.0%; Pred. No. 2.8e-29;
Matches 62; Conservative 16; Mismatches 20; Indels 2; Gaps 2;
```

QY 10 TSLSPGERATLSQASQSI-SNHLHWYQORPGQAPRLIXYSQSISGIPARFSGSGG 68  
 Db 2 TMAASPGKITITCSASSSISSNLYHWYQKPGFSPKLLIYRTSNLASGVPTFSGSGG 61  
 QY 69 TDTLTLSLEPEDFAVYQCQSGSWP-HTFGGKVEIK 107  
 Db 62 TSYSLTIGTMEADVATYQCQSGSSIPRYTFGGTKLEIK 101

RESULT 15

O9ERZ9  
 ID O9ERZ9 PRELIMINARY; PRT; 107 AA.  
 AC O9ERZ9;  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)  
 DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
 RT "Cloning and sequencing of the light chain fragment of variable region  
 RT genes of an anti-TNF-a monoclonal antibody.";  
 RL J. Cell. Mol. Immunol. 12:21-26(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
 RT "Construction and sequencing of the single-chain antibody gene of a  
 RT human TNF-alpha specific monoclonal antibody.";  
 RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF262753; AAG23804.1; -;  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA604A26C3 CRC64;

Query Match 56.6%; Score 315; DB 11; Length 107;  
 Best Local Similarity 54.2%; Pred. No. 5.1e-28;  
 Matches 58; Conservative 22; Mismatches 21; Indels 6; Gaps 1;  
 QY 4 LTQSPATLSLSPGERATLSQASQSI-----SNHLHWYQORPGQAPRLIXYSQSISG 57  
 Db 1 MTQSPSLANSVQKVTMSCKSSQSVLNSNTQKNYLAHQKPGQSPPELLVYFSTRSG 60  
 QY 58 IPARFSGSGGTDFTLTISLEPEDFAVYQCQSGSWPHTFGGKTV 104  
 Db 61 VPDRFMGSGGTDFTLTISVQTDLDYFCQGHYRTPTFGSGTKL 107

Search completed: October 11, 2001, 12:07:35  
 Job time: 410 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2001, 12:01:58 ; Search time 44.8 Seconds  
(without alignments)  
144.794 Million cell updates/sec

Title: US-08-791-391a-32

Perfect score: 557

Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHFGGTRKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	555	99.6	107	AAW76006	LM609 grafted anti
2	555	99.6	107	AAW76002	Vitaxin antibody 1
3	555	99.6	107	AAB61360	Vitaxin light chal
4	555	99.6	107	AAB61364	Light chain variab
5	506	90.8	107	AAW25729	Humanised VL regio
6	506	90.8	107	AAW25729	Humanised CMV5 ant
7	506	90.8	107	AAW25729	Humanised CMV5 ant
8	504	90.5	107	AAW25729	Humanised anti-alp
9	504	90.5	112	AAW84100	Vitronectin alpha
10	501	89.9	127	AAW08946	Kappa light chain
11	495	88.9	107	AAW08948	Kappa light chain

12	495	88.9	107	18	AAW08949	Kappa light chain
13	490	88.0	107	20	AAW30205	The variable light
14	489	87.8	107	20	AAW30203	The variable light
15	484	86.9	127	21	AAW32407	Mouse anti-verotox
16	480	86.2	127	15	AAW50192	Light chain variab
17	480	86.2	127	20	AAW26982	Light chain variab
18	478	85.8	107	14	AAW37612	hIL2R Ab L chain v
19	477	85.6	107	21	AAW71240	Humanised antibody
20	474	85.1	107	21	AAW70604	Vkappa region of h
21	474	85.1	127	15	AAW50187	Light chain variab
22	474	85.1	127	20	AAW26980	Light chain variab
23	474	85.1	245	21	AAW70605	scfv fragment of h
24	471	84.6	127	15	AAW50191	Light chain variab
25	471	84.6	127	20	AAW26981	Light chain variab
26	464	83.3	107	19	AAW76004	LM609 antibody lig
27	464	83.3	107	22	AAB61362	Antibody LM609 lig
28	455	81.7	107	22	AAB66414	Human Fab clone LD
29	453	81.3	107	21	AAW71238	Humanised antibody
30	450.5	80.9	108	22	AAB72884	Human anti-HER2/ne
31	450	80.8	105	20	AAW87456	Jk gene product.
32	450	80.8	105	20	AAW87458	Humanised anti-alp
33	449.5	80.7	107	18	AAW24513	Anti-Factor-IX hum
34	449	80.6	109	20	AAW06380	Murine monoclonal
35	446	80.1	214	20	AAW08599	Anti-human TNF-alp
36	441	79.2	107	22	AAB69677	Murine CMV5 antibo
37	441	79.2	127	22	AAB69687	Murine CMV5 antibo
38	440	79.0	349	12	AAW12128	1B1 IgG aberrant 1
39	440	79.0	401	12	AAW12129	ORF 1 of IgG light
40	440	79.0	414	12	AAW13111	1B1 IgG aberrant 1
41	440	79.0	414	12	AAW13018	1B1 IgG aberrant 1
42	438.5	78.7	109	22	AAB62756	Human HIV-1 monocl
43	438	78.6	127	15	AAW54093	Sequence of mouse
44	436.5	78.4	108	21	AAW53774	VL component of an
45	436.5	78.4	238	21	AAW53775	An antibody with i

#### ALIGNMENTS

RESULT 1

AAW76006

ID AAW76006 standard; Protein; 107 AA.

XX

AC AAW76006;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody light chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

Key Location/Qualifiers

FT Misc-difference 49

FT /label= Arg, Met

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.  
 DR N-PSDB; AAV49843.  
 XX  
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 XX Claim 19; Fig 7; 129pp; English.  
 XX  
 CC This sequence represents a LM609 grafted antibody variable light chain  
 CC region. LM609 and the antibody vitaxin bind selectively to integrin  
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand  
 CC and thus block integrin-mediated signal transduction. This is useful in  
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX  
 XX Sequence 107 AA;  
 SQ

Query Match 99.6%; Score 555; DB 19; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60  
 |||||  
 Db 1 eivltqspatislspgeratlsqasqisnlnhwyqrpqgprlllyrsgisgipa 60  
 |||||

QY 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107  
 |||||  
 Db 61 rfsqsgsgdtftltisslepedfavycqsgswphtfggktveik 107  
 |||||

RESULT 2  
 AAW76002  
 ID AAW76002 standard; Protein; 107 AA.  
 XX  
 AC AAW76002;  
 XX  
 XX 02-NOV-1998 (first entry)  
 DT  
 DE Vitaxin antibody light chain variable region protein fragment.  
 XX  
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis.  
 XX  
 XX Mus sp.  
 OS  
 XX WO9833919-A2.  
 PN  
 XX 06-AUG-1998.  
 PD  
 XX 30-JAN-1998; 98WO-US01826.  
 PF  
 XX 30-JAN-1997; 97US-0791391.  
 PR  
 XX (IXSY-) IXSYS INC.  
 PA  
 XX Glaser SM, Huse WD;  
 PI  
 XX WPI; 1998-437472/37.  
 DR N-PSDB; AAV49821.  
 DR  
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 XX Claim 1; Fig 1b; 129pp; English.  
 XX  
 CC This sequence represents the vitaxin antibody variable light chain  
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin  
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a  
 CC ligand and thus block integrin-mediated signal transduction. This is  
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated  
 CC disease, specifically angiogenesis and restenosis (but also e.g.  
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,  
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,  
 CC osteoporosis etc.). The antibodies contain non-murine framework regions  
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity  
 CC more than 90 times greater than that of parent the parent antibody.  
 XX  
 XX Sequence 107 AA;  
 SQ

Query Match 99.6%; Score 555; DB 19; Length 107;  
 Best Local Similarity 99.1%; Pred. No. 3.7e-36;  
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSOSISGIPA 60  
 |||||  
 Db 1 eivltqspatislspgeratlsqasqisnlnhwyqrpqgprlllyrsgisgipa 60  
 |||||

QY 61 RFSGSGGDTFTLTISLLEPEDFAVYCCQSGSWPHTFGGKTVEIK 107  
 |||||  
 Db 61 rfsqsgsgdtftltisslepedfavycqsgswphtfggktveik 107  
 |||||

RESULT 3  
 AAB61360  
 ID AAB61360 standard; protein; 107 AA.  
 XX  
 AC AAB61360;  
 XX  
 XX 03-APR-2001 (first entry)  
 DT  
 XX Vitaxin light chain variable region protein.  
 DE  
 XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200078815-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 23-JUN-2000; 2000WO-US17454.  
 PF  
 XX 24-JUN-1999; 99US-0339922.  
 PR  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 XX Huse WD, Wu H;  
 XX  
 XX WPI; 2001-050110/06.  
 DR  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 XX Disclosure; Fig 1; 132pp; English.  
 PS  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.  
XX  
SQ Sequence 107 AA;

Query Match 99.6%; Score 555; DB 22; Length 107;  
Best Local Similarity 99.1%; Pred. No. 3.7e-36;  
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60  
DB 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60  
QY 61 RFSGSGSGTDFTLTISLPEPEFAYVYCOQSGSWPHTFGGKVEIK 107  
DB 61 RFSGSGSGTDFTLTISLPEPEFAYVYCOQSGSWPHTFGGKVEIK 107

RESULT 4

AAB61364  
ID AAB61364 standard; protein; 107 AA.

XX AC AAB61364;

XX DT 03-APR-2001 (first entry)

XX DE Light chain variable region of LM609.

XX KW LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
XX inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
XX to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of  
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
XX osteoporosis -

XX PS Disclosure; Fig 7; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
XX exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
XX their functional fragments. The antibodies or their functional  
XX fragments can be used in the diagnosis and treatment of  
XX alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
XX diseases (such as psoriasis and chronic articular rheumatism),  
XX disorders associated with inappropriate or inopportune invasion of  
XX vessels (such as diabetic retinopathy, neovascular glaucoma and  
XX cancer disorders such as tumours and Kaposi's sarcoma), retinal  
XX diseases (such as macular degeneration), restenosis and  
XX osteoporosis.

XX SQ Sequence 107 AA;

Query Match 99.6%; Score 555; DB 22; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.7e-36;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60  
DB 1 EIVLTQSPATLSLSPGERATLSCQASQTSNHLHWYQQRPQAPRLILXYRQSISGIPA 60  
QY 61 RFSGSGSGTDFTLTISLPEPEFAYVYCOQSGSWPHTFGGKVEIK 107  
DB 61 RFSGSGSGTDFTLTISLPEPEFAYVYCOQSGSWPHTFGGKVEIK 107

RESULT 5

AAR25729  
ID AAR25729 standard; Protein; 107 AA.

XX AC AAR25729;

XX DT 13-JAN-1993 (first entry)

XX DE Humanised VL region of the mouse CMV5 antibody.

XX KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;  
XX GH; light chain; variable region; framework; human; Wol.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
XX Region 24..34  
XX /note= "CDR"

XX FT Region 50..56  
XX /note= "CDR"

XX FT Region 89..97  
XX /note= "CDR"

XX FT Misc-difference 49  
XX /note= "mutated residue"

XX PN WO9211018-A.

XX PD 09-JUL-1992.

XX PF 19-DEC-1991; 91WO-US09711.

XX PR 19-DEC-1990; 90US-0634278.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Co MS, Coelingh KL, Landolfi NF, Queen CL, Schneider WP;

XX DR WPI; 1992-249842/30.

XX PT New immunoglobulin(s) having murine CDRs in human framework  
XX regions - have lower antigenicity; useful for treating e.g. HSV,  
XX CMV, T-cell disorders, myeloid disorders and auto-immune  
XX conditions

XX PS Claim 40; Fig 27A; 141pp; English.

XX CC The sequence shows the humanised mature light chain variable  
XX region of the mouse CMV5 antibody. Murine CDRs were used  
XX in a human Wol framework to produce a pure humanised immunoglobulin  
XX (Ig) which is capable of binding to the GH glycoprotein of  
XX cytomegalovirus. The Ig is non immunogenic, due to the human  
XX framework, and has a strong affinity for its predetermined  
XX antigen. They can be produced in large quantities via recombinant  
XX DNA and monoclonal antibody technology. The humanised Igs may be  
XX used alone or in combination with chemotherapeutic agents such as  
XX non-steroidal anti-inflammatory drugs or immunosuppressants.

XX CC See also AAR25721-32.

XX

SQ Sequence 107 AA; Query Match 90.8%; Score 506; DB 13; Length 107;  
Best Local Similarity 90.7%; Pred. No. 2.2e-32;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATISLCASQSIINHLHWYQQRPQAPRLILXYRSQSISGIPA 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 eivltqspgtlslspgeratlsrscasqsinnhlhwyyqqkpgqaprlilkyasqisigpd 60

QY 61 RFSGSGSTDTFTLTISLEPEDFAVYYCQSGSWPHTFGGTKEIK 107  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 rfssgsgtftltisrlepavedfavyycqsgswphtfggktkeik 107

RESULT 6  
AAB69678  
ID AAB69678 standard; Protein; 107 AA.  
XX  
AC AAB69678;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human CMV5 antibody light chain SEQ ID NO: 63.  
XX  
KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;  
light chain; graft versus host disease; transplant; autoimmune disease;  
multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;  
myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

OS Mus sp.  
OS Homo sapiens.  
PN US6180370-B1.  
XX  
PD 30-JAN-2001.  
XX  
PF 07-JUN-1995; 95US-0484537.  
XX  
PR 28-DEC-1988; 88US-0290975.  
PR 13-FEB-1989; 89US-0310252.  
PR 28-SEP-1990; 90US-0590274.  
PR 19-DEC-1990; 90US-0634278.  
XX  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
PI Queen CL, Selick HE;  
XX  
DR WPI; 2001-190856/19.  
XX  
PT Producing humanized immunoglobulin, involves producing a cell  
containing DNA segments encoding humanized heavy and light chain  
variable regions, and expressing the DNA segments in the cell -  
Disclosure; Fig 6; 145pp; English.

The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of

CC graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections and myeloid leukaemia. The present sequence is an antibody used to demonstrate the method of the invention.

SQ Sequence 107 AA;

Query Match 90.8%; Score 506; DB 22; Length 107;  
Best Local Similarity 90.7%; Pred. No. 2.2e-32;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATISLCASQSIINHLHWYQQRPQAPRLILXYRSQSISGIPA 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 eivltqspgtlslspgeratlsrscasqsinnhlhwyyqqkpgqaprlilkyasqisigpd 60

QY 61 RFSGSGSTDTFTLTISLEPEDFAVYYCQSGSWPHTFGGTKEIK 107  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 rfssgsgtftltisrlepavedfavyycqsgswphtfggktkeik 107

RESULT 6  
AAB69678  
ID AAB69678 standard; Protein; 107 AA.  
XX  
AC AAB69678;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;  
light chain; graft versus host disease; transplant; autoimmune disease;  
multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;  
myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

OS Mus sp.  
OS Homo sapiens.  
PN US6180370-B1.  
XX  
PD 30-JAN-2001.  
XX  
PF 07-JUN-1995; 95US-0484537.  
XX  
PR 28-DEC-1988; 88US-0290975.  
PR 13-FEB-1989; 89US-0310252.  
PR 28-SEP-1990; 90US-0590274.  
PR 19-DEC-1990; 90US-0634278.  
XX  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
PI Queen CL, Selick HE;  
XX  
DR WPI; 2001-190856/19.  
XX  
PT Producing humanized immunoglobulin, involves producing a cell  
containing DNA segments encoding humanized heavy and light chain  
variable regions, and expressing the DNA segments in the cell -  
Disclosure; Fig 6; 145pp; English.

The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of

CC graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections and myeloid leukaemia. The present sequence is an antibody used to demonstrate the method of the invention.

SQ Sequence 107 AA;

Query Match 90.8%; Score 506; DB 22; Length 107;  
Best Local Similarity 90.7%; Pred. No. 2.2e-32;







SQ Sequence 107 AA;

Query Match 88.9%; Score 495; DB 18; Length 107;  
 Best Local Similarity 87.9%; Pred. No. 1.5e-31;  
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60

QY 61 RFGSGSGTDFLTITISLPEPFAVYCYQSGSWPHTFGGKVEIK 107  
 DB 61 RFGSGSGTDFLTITISLPEPFAVYCYQSGSWPHTFGGKVEIK 107

RESULT 12  
 AAW08949  
 ID AAW08949 standard; Protein; 107 AA.  
 XX  
 AC AAW08949;  
 DT 18-SEP-1997 (first entry)  
 XX  
 DE Kappa light chain variable region of 225RB antibody.  
 KW Kappa; light chain; reshaped; monoclonal; antibody; 225RB;  
 KW human; epidermal growth factor; EGF; receptor; inhibition; growth;  
 KW tumour; cell; late stage; prostatic; prostate; variable region;  
 KW framework; complementarity determining region; CDR.  
 XX  
 OS Homo sapiens.  
 PH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= framework\_1  
 FT Region 24..34  
 FT /label= CDR\_1  
 FT Region 35..49  
 FT /label= framework\_2  
 FT Region 50..56  
 FT /label= CDR\_2  
 FT Region 57..88  
 FT /label= framework\_3  
 FT Region 89..97  
 FT /label= CDR\_3  
 FT Region 98..107  
 FT /label= framework\_4  
 XX  
 PN WO9640210-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96WO-US09847.  
 XX  
 PR 15-DEC-1995; 95US-0573289.  
 PR 07-JUN-1995; 95US-0482982.  
 XX  
 PA (IMCL-) IMCLONE SYSTEMS INC.  
 PA (MRCC-) MRC COLLABORATIVE CENT.  
 XX  
 PI Giorgio NA, Goldstein NI, Jones ST, Saldanha JW;  
 XX  
 DR WPI; 1997-051897/05.  
 XX  
 PT Chimeric and humanised versions of anti-EGF receptor antibody 225 -  
 PT used for inhibiting tumour growth, esp. of late stage prostatic  
 PT tumour  
 XX  
 PS Claim 29; Fig 21; 112pp; English.  
 XX  
 CC The present sequence is the kappa light chain variable region  
 CC of the reshaped human monoclonal antibody (MAB) H225, 225RKA. The

CC MAB is specific for the human epidermal growth factor (EGF)  
 CC receptor.  
 CC The MAB, or a fragment, can be used to inhibit the growth of tumour  
 CC cells, especially late stage prostatic tumour cells in humans,  
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,  
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle  
 CC inhibitor.  
 CC  
 SQ Sequence 107 AA;

Query Match 88.9%; Score 495; DB 18; Length 107;  
 Best Local Similarity 87.9%; Pred. No. 1.5e-31;  
 Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60  
 DB 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLIIYRQSISGIPA 60

QY 61 RFGSGSGTDFLTITISLPEPFAVYCYQSGSWPHTFGGKVEIK 107  
 DB 61 RFGSGSGTDFLTITISLPEPFAVYCYQSGSWPHTFGGKVEIK 107

RESULT 13  
 AAY30205  
 ID AAY30205 standard; Protein; 107 AA.  
 XX  
 AC AAY30205;  
 DT 01-NOV-1999 (first entry)  
 XX  
 DE The variable light chain of humanised antibody L3.17.  
 KW Light chain variable region; chimeric antibody; anti-CD40 antibody;  
 KW chi220; humoral immune response; T cell dependent antigen;  
 KW collagen induced arthritis; transplant induced rejection;  
 KW T cell mediated disorder; autoimmune disease; inflammatory disease;  
 KW transplantation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9942075-A2.  
 XX  
 PD 26-AUG-1999.  
 XX  
 PF 10-FEB-1999; 99WO-US02949.  
 XX  
 PR 19-FEB-1998; 98US-0026291.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;  
 PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;  
 XX  
 DR WPI; 1999-527408/44.  
 DR N-PSDB; AAZ10205.  
 XX  
 PT Antibody that binds human CD40, for treating T cell mediated  
 PT disorders  
 XX  
 PS Claim 26; Page 33-34; 77pp; English.  
 XX  
 CC The present sequence represents the variable light chain of humanised  
 CC antibody L3.17. The antibody is effective in modulating humoral immune  
 CC response against T cell dependent antigens, collagen induced arthritis  
 CC and transplant induced rejection. They are also useful for their  
 CC anti-inflammatory properties. The antibodies have wide therapeutic  
 CC applications, including autoimmune and inflammatory diseases and  
 CC transplantation. The antibody can be used in a pharmaceutical composition  
 CC for treating a patient suffering from a T cell mediated disorder. They  
 CC can also be used to treat autoimmune diseases, inflammatory diseases,

CC and transplantation.  
XX Sequence 107 AA;  
SQ

Query Match 88.0%; Score 490; DB 20; Length 107;  
Best Local Similarity 88.8%; Pred. No. 3.7e-31;  
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGAPRLIIXYRSQISGIPA 60  
Db 1 elvltqspatlsispgeratlsqrasgsisdylhwqkpgqprlliyashsisgipa 60  
QY 61 RFGSGSGDTFTLTISLEPEDFAVYCCQSGSWPHFTFGGKTVEIK 107  
Db 61 rfgsgsgdtftltisslepedfavycqghgsypwtfgggtkveik 107

RESULT 14  
AAV3203  
ID AAY30203 standard; Protein; 107 AA.  
XX  
AC AAY30203;  
XX  
XX 01-NOV-1999 (first entry)  
DT  
DE The variable light chain of humanised antibody F4.  
XX  
XX Light chain variable region; chimeric antibody; anti-CD40 antibody;  
KW chi220; humoral immune response; T cell dependent antigen;  
KW collagen induced arthritis; transplant induced rejection;  
KW T cell mediated disorder; autoimmune disease; inflammatory disease;  
KW transplantation.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
XX WO942075-A2.  
PN  
XX 26-AUG-1999.  
PD  
XX 10-FEB-1999; 99WO-US02949.  
PF  
XX 19-FEB-1998; 98US-0026291.  
PR  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA  
XX Aruffo AA, Bajorath J, Berry KK, Harris LJ, Hollenbaugh D;  
PI Huse WD, Sladak AW, Thorne BA, Watkins JD, Wu H;  
PI  
XX WPI; 1999-527408/44.  
DR N-PSDB; AA210203.  
DR  
XX Antibody that binds human CD40, for treating T cell mediated disorders  
PT  
XX  
PS Claim 21; Page 32-33; 77pp; English.

The present sequence represents the variable light chain of humanised antibody F4. The antibody is effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases,  
XX  
SQ Sequence 107 AA;

Query Match 87.8%; Score 489; DB 20; Length 107;

Best Local Similarity 88.8%; Pred. No. 4.4e-31;  
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGAPRLIIXYRSQISGIPA 60  
Db 1 elvltqspatlsispgeratlsqrasgsisdylhwqkpgqprlliyashsisgipa 60  
QY 61 RFGSGSGDTFTLTISLEPEDFAVYCCQSGSWPHFTFGGKTVEIK 107  
Db 61 rfgsgsgdtftltisslepedfavycqghgsfpwtfgggtkveik 107  
RESULT 15  
AAV32407  
ID AAY32407 standard; Protein; 127 AA.  
XX  
AC AAY32407;  
XX  
XX 13-MAR-2000 (first entry)  
DT  
DE Mouse anti-verotoxin II antibody Vtm1-1 humanised VL region.  
XX  
KW Verotoxin II; VT2; shiga-like toxin; Vtm1-1; MuVtm1-1;  
KW monoclonal antibody; light chain; mouse; humanised antibody; human;  
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
KW HUS; therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX Key  
FH Peptide  
FT 1..20  
FT /note= "signal peptide"  
FT Protein  
FT 21..127  
FT /note= "mature protein"  
FT 44..54  
FT Region  
FT /note= "complementarity determining region 1"  
FT 70..76  
FT Region  
FT /note= "complementarity determining region 2"  
FT 109..117  
FT Region  
FT /note= "complementarity determining region 3"  
XX  
XX WO959629-A1.  
PN  
XX 25-NOV-1999.  
PD  
XX 19-MAY-1999; 99WO-US11179.  
PF  
XX 20-MAY-1998; 98US-0086570.  
PR  
XX (TEIJ ) TEIJIN LTD.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;  
PI  
XX WPI; 2000-086580/07.  
DR N-PSDB; AA235244.  
DR  
XX Humanized antibody binding to verotoxin II used for treating verotoxin producing E. coli -  
XX  
XX Claim 12; Fig 2b; 59pp; English.  
PS  
XX This sequence represents a humanised light chain variable region of murine monoclonal antibody Vtm1-1 (MuVtm1-1), an antibody that specifically binds to the B subunit of verotoxin II (VT2). The invention relates to humanised antibodies against VT2 that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVtm1-1 comprising the complementarity determining regions of MuVtm1-1 and the heavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain frameworks, provided that at least 1 position selected from L49, H29, H30, H49 and H98 is occupied by the amino acid at the equivalent

CC position of the MuVtm1-1 antibody heavy or light chain variable region  
CC framework. Such humanized antibodies have an affinity for VT2 that is  
CC 3-, 5 or 10-times that of MuVtm1-1. They are used for treating a  
CC patient suffering from, or at risk of, the toxic effects from VT2  
CC (claimed), especially for treating verotoxin producing Escherichia  
CC coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).

XX  
SQ Sequence 127 AA;

Query Match 86.9%; Score 484; DB 21; Length 127;  
Best Local Similarity 88.8%; Pred. No. 1.2e-30;  
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQISGIPA 60  
|||  
DB 21 eivltqspatlsvspgeratlsqrasqtisnlnhwyqkpgqaprllikasqsisgipa 80  
|||  
QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||  
DB 81 rfsgsgsgtdftltislesedfavyycqsyswpltfgggtkveik 127  
|||

Search completed: October 11, 2001, 12:01:58  
Job time: 968 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw.model

Run on: October 11, 2001, 12:06:42 ; Search time 239.24 Seconds  
(without alignments)  
99.221 Million cell updates/sec

Title: US-08-791-391A-32  
Perfect score: 557  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....CQSGSWPHFGGTRKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues  
Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	99.6	107	11 US-08-790-540-4	Sequence 4, Appli
2	555	99.6	107	11 US-08-790-540A-4	Sequence 4, Appli
3	555	99.6	107	11 US-08-791-391-4	Sequence 4, Appli
4	555	99.6	107	11 US-08-791-391-32	Sequence 32, Appl
5	555	99.6	107	11 US-08-791-391A-4	Sequence 4, Appli
6	555	99.6	107	11 US-08-791-391A-32	Sequence 32, Appl
7	555	99.6	107	14 US-09-016-061-4	Sequence 4, Appli
8	555	99.6	107	14 US-09-016-061-32	Sequence 32, Appl
9	555	99.6	107	17 US-09-339-922A-4	Sequence 4, Appli
10	555	99.6	107	17 US-09-339-922A-32	Sequence 32, Appl

11	506	90.8	107	17	US-09-325-000-22	Sequence 22, Appl
12	504	90.5	107	1	PCT-US98-04987-10	Sequence 10, Appl
13	504	90.5	107	17	US-09-380-910-10	Sequence 10, Appl
14	504	90.5	112	1	PCT-US98-04987-14	Sequence 14, Appl
15	504	90.5	112	17	US-09-380-910-14	Sequence 14, Appl
16	501	89.9	127	13	US-08-973-065A-17	Sequence 17, Appl
17	501	89.9	127	13	US-08-973-065B-17	Sequence 17, Appl
18	495	88.9	107	13	US-08-973-065B-114	Sequence 114, App
19	490	88.0	107	1	PCT-US99-02949-12	Sequence 12, Appl
20	490	88.0	107	14	US-09-026-291-12	Sequence 12, Appl
21	490	88.0	107	16	US-09-247-352-12	Sequence 12, Appl
22	489	87.8	107	1	PCT-US99-02949-8	Sequence 8, Appli
23	489	87.8	107	14	US-09-026-291-8	Sequence 8, Appli
24	489	87.8	107	16	US-09-247-352-8	Sequence 8, Appli
25	483	86.7	107	13	US-08-973-065B-113	Sequence 113, App
26	482	86.5	113	13	US-08-973-065A-22	Sequence 22, Appl
27	482	86.5	113	13	US-08-973-065A-23	Sequence 23, Appl
28	482	86.5	113	13	US-08-973-065B-22	Sequence 22, Appl
29	482	86.5	113	13	US-08-973-065B-23	Sequence 23, Appl
30	480	86.2	127	5	US-08-127-721-10	Sequence 10, Appl
31	480	86.2	127	8	US-08-476-176-10	Sequence 10, Appl
32	480	86.2	127	8	US-08-485-246-10	Sequence 10, Appl
33	478	85.8	107	6	US-08-232-081-9	Sequence 9, Appli
34	478	85.8	107	6	US-08-232-081A-9	Sequence 9, Appli
35	477	85.6	107	18	US-09-438-954-3	Sequence 3, Appli
36	474	85.1	107	1	PCT-US99-21646-25	Sequence 25, Appl
37	474	85.1	107	17	US-09-397-569-25	Sequence 25, Appl
38	474	85.1	127	5	US-08-127-721-6	Sequence 6, Appli
39	474	85.1	127	8	US-08-476-176-6	Sequence 6, Appli
40	474	85.1	127	8	US-08-485-246-6	Sequence 6, Appli
41	474	85.1	245	1	PCT-US99-21646-27	Sequence 27, Appl
42	474	85.1	245	17	US-09-397-569-27	Sequence 27, Appl
43	471	84.6	127	5	US-08-127-721-8	Sequence 8, Appli
44	471	84.6	127	8	US-08-476-176-8	Sequence 8, Appli
45	471	84.6	127	8	US-08-485-246-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-08-790-540-4  
; Sequence 4, Application US/08790540  
; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; STREET: Campbell & Flores LLP  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/790,540  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IX 2405  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:



4.

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/791.391  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 1482  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-791-391-32

Query Match 99.6%; Score 555; DB 11; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60  
|||||  
Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60  
|||||

Qy 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||||  
Db 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||||

RESULT 5

US-08-791-391a-4  
; Sequence 4, Application US/08791391A  
; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/791.391A  
; FILING DATE: 30-JAN-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IX 1482  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-791-391A-4

Query Match 99.6%; Score 555; DB 11; Length 107;  
Best Local Similarity 99.1%; Pred. No. 5.5e-49;  
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60  
|||||  
Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60  
|||||

Qy 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||||  
Db 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||||

RESULT 6

US-08-791-391A-32  
; Sequence 32, Application US/08791391A  
; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/791.391A  
; FILING DATE: 30-JAN-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IX 1482  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-791-391A-32

Query Match 99.6%; Score 555; DB 11; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60  
|||||  
Db 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQSIGIPA 60  
|||||

Qy 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||||  
Db 61 RFSGSGSGTDFTLTISLLEPEDFAVYYCQSGSWPHTFGGKVEIK 107  
|||||

RESULT 7

US-09-016-061-4  
; Sequence 4, Application US/09016061





RESULT 10  
US-09-339-922A-32  
; Sequence 32, Application US/09339922A  
; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic  
; FILE REFERENCE: P-IX 3536  
; CURRENT APPLICATION NUMBER: US/09/339,922A  
; CURRENT FILING DATE: 1999-06-24  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (49)  
; OTHER INFORMATION: Xaa - Arg or Met  
; OTHER INFORMATION: Description of Artificial Sequence: grafted  
; OTHER INFORMATION: antibody variable region  
US-09-339-922A-32

Query Match 99.6%; Score 555; DB 17; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.5e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIVLQSPATLSLSPGERATLSCQASQISNLHWYQORPGQAPRLLIYRQSISGIPA 60  
DB 1 EIVLQSPATLSLSPGERATLSCQASQISNLHWYQORPGQAPRLLIYRQSISGIPA 60  
QY 61 RPSGSGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107  
DB 61 RPSGSGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107

RESULT 11  
US-09-325-000-22  
; Sequence 22, Application US/09325000  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William P.  
; APPLICANT: Landolfi, Nicholas F.  
; APPLICANT: Coelingh, Kathleen L.  
; APPLICANT: Sellick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/325,000  
; FILING DATE: 01-JUN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252

; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,537  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-002650US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-325-000-22

Query Match 90.8%; Score 506; DB 17; Length 107;  
Best Local Similarity 90.7%; Pred. No. 6e-44;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLQSPATLSLSPGERATLSCQASQISNLHWYQORPGQAPRLLIYRQSISGIPA 60  
DB 1 EIVLQSPCTLSLSPGERATLSCRASQISNLHWYQKPGQAPRLLIYRQSISGIPD 60  
QY 61 RPSGSGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107  
DB 61 RPSGSGTDFTLTISLLEPEDFAVYCYQSGSWPHTFGGKVEIK 107

RESULT 12  
PCT-US98-04987-10  
; Sequence 10, Application PC/TUS9804987  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Johanson, Kyung O.  
; APPLICANT: Taylor, Alexander H.  
; TITLE OF INVENTION: Humanized Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/04987  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/039,609  
; FILING DATE: 12 March 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T.  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: P50629-1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4800  
TELEFAX: 610-270-4026  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US98-04987-10

Query Match 90.5%; Score 504; DB 1; Length 107;  
Best Local Similarity 89.7%; Pred. No. 9.7e-44;  
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQISGIPA 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQKPGQAPRLLIKVASQISGIPS 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 RFSGSGGTDTLTISLSEPEFAVYCCQSGSWPHTFGGKVEIK 107  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 61 RFSGSGGTDTLTISRLEPEFAVYCCQSGNSWPTFGGKVEIK 107

RESULT 13  
US-09-380-910-10  
; Sequence 10, Application US/09380910  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; Jonak, Zdenka L.  
; Taylor, Alexander H.  
; TITLE OF INVENTION: Humanized Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/380,910  
; FILING DATE: 24-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/039,609  
; FILING DATE: 12 March 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T.  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: P50629  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5015  
; TELEFAX: 610-270-5090  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-380-910-10

Query Match 90.5%; Score 504; DB 17; Length 107;  
Best Local Similarity 89.7%; Pred. No. 9.7e-44;

Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQISGIPA 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQKPGQAPRLLIKVASQISGIPS 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 RFSGSGGTDTLTISLSEPEFAVYCCQSGSWPHTFGGKVEIK 107  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 61 RFSGSGGTDTLTISRLEPEFAVYCCQSGNSWPTFGGKVEIK 107

RESULT 14  
PCT-US98-04987-14  
; Sequence 14, Application PC/TUS9804987  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Johanson, Kyung O.  
; APPLICANT: Taylor, Alexander H.  
; TITLE OF INVENTION: Humanized Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/04987  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/039,609  
; FILING DATE: 12 March 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T.  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: P50629-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4800  
; TELEFAX: 610-270-4026  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US98-04987-14

Query Match 90.5%; Score 504; DB 1; Length 112;  
Best Local Similarity 89.7%; Pred. No. 1e-43;  
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQORPGQAPRLLIYRSQISGIPA 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQKPGQAPRLLIKVASQISGIPS 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 RFSGSGGTDTLTISLSEPEFAVYCCQSGSWPHTFGGKVEIK 107  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 61 RFSGSGGTDTLTISRLEPEFAVYCCQSGNSWPTFGGKVEIK 107

RESULT 15  
US-09-380-910-14  
; Sequence 14, Application US/09380910  
; GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation  
Jonak, Zdenka L.  
Johanson, Kyung O.  
Taylor, Alexander H.  
TITLE OF INVENTION: Humanized Monoclonal Antibodies  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/380,910  
FILING DATE: 24-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/039,609  
FILING DATE: 12 March 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: P50629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5015  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-380-910-14

Query Match 90.5%; Score 504; DB 17; Length 112;  
Best Local Similarity 89.7%; Pred. No. 1e-43;  
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQRPQGPAPRLILYRSQISGIPA 60  
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
1 DIVLTQSPGTLSPGERATLSCRASQISNHLHWYQRPQGPAPRLILYRSQISGIPS 60  
QY 61 RFGSGSGTDFLTITSLLEPEDFAVYCCQSGSWPHTFGGKVEIK 107  
DB :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :  
61 RFGSGSGTDFLTITSLRLEPEDFAVYCCQSGSWPHTFGGKVEIK 107

Search completed: October 11, 2001, 12:06:42  
Job time: 397 sec

**THIS PAGE BLANK (USPTO)**